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OM protein - protein search, using sw model

Run on: April 19, 2005, 16:23:17 ; Search time 121.992 Seconds

(without alignments)  
779.913 Million cell updates/sec

Title: US-09-250-056b-1

Perfect score: 1300

Sequence: 1 QVQLVSGGGLVQPGSURL.....YDSLSGWVFGGKTLTVLG 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: A\_Geneseq\_16Dec04:\*  
2: geneseqp19808:\*  
3: geneseqp19908:\*  
4: geneseqp20008:\*  
5: geneseqp20018:\*  
6: geneseqp20028:\*  
7: geneseqp20038:\*  
8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1300	100.0	246	3	AA58235 Internal
2	1292	99.4	291	8	ADN06985 Human EFG
3	1292	99.4	291	8	ADN06984 Human EFG
4	1135.5	87.3	245	8	ADS09287 Human C-M
5	1135.5	87.1	251	8	ADSI2384 Human IGF
6	1125.5	86.6	247	5	ABP45881 Human Bly
7	1125.5	86.6	247	7	ADG96708 Single ch
8	1121.5	86.3	258	8	ADS92884 Human Myo
9	1115	85.8	248	8	ADIS8091 Reg IV-SP
10	1113.5	85.7	247	5	ABP45967 Human Bly
11	1113.5	85.7	247	7	ADG96794 Single ch
12	1108	85.2	248	8	ADIS8045 Reg IV-SP
13	1096.5	84.3	258	8	ADSI2872 Human Myo
14	1092.5	84.0	247	5	ABP45942 Human Bly
15	1092.5	84.0	247	7	ADG96769 Single ch
16	1092.5	84.0	249	8	ADIS8094 Reg IV-SP
17	1092	84.0	252	5	ABP45508 Human Bly
18	1092	84.0	252	7	ADG96335 Single ch
19	1086	83.5	277	8	ADSI2150 Melanoma
20	1086	83.4	238	8	ADSI2139 Human c-M
21	1082.5	83.3	245	8	ADSI2139 Human c-M
22	1081	83.2	252	5	ABP45351 Human Bly
23	1081	83.2	252	7	ADG96178 Single ch
24	1080	83.1	258	5	ABP45830 Human Bly
25	1080	83.1	258	7	ADG96657 Single ch

26	1076.5	82.8	243	5	ABP45958 Human Bly
27	1076.5	82.8	243	7	ADG96785 Single ch
28	1075.5	82.7	310	2	AAW83324 Single ch
29	1075.5	82.7	310	5	ABP09605 Amino aci
30	1075.5	82.7	310	6	ABG74386 Single ch
31	1075.5	82.7	310	7	ADG98739 Human sin
32	1075.5	82.7	310	8	ADSI2139 Human sin
33	1069	82.2	240	3	AAV15124 Anti-huma
34	1069	82.2	240	3	AAV15125 Anti-muri
35	1069	82.2	252	5	ABP45190 Human Bly
36	1069	82.2	252	7	ADG96017 Single ch
37	1065.5	82.0	262	8	ADSI2866 Human Myo
38	1062	81.7	250	5	ABP45409 Human Bly
39	1062	81.7	250	7	ADG96236 Single ch
40	1059.5	81.5	253	6	ABJ19830 Human VEG
41	1059.5	81.5	253	8	ADH13872 Human vas
42	1056	81.2	246	6	ABJ19834 Human VEG
43	1056	81.2	246	6	ADH13876 Human vas
44	1053.5	81.0	243	8	ADSI2864 Human c-M
45	1053	81.0	248	8	ADSI2865 Reg IV-SP

## ALIGNMENTS

RESULT 1	AA58235	standard; protein; 246 aa.
ID	AA58235	standard; protein; 246 aa.
XX	AA58235	
AC	AA58235	
XX	AA58235	
DT	27-MAR-2000	(first entry)
XX	27-MAR-2000	(first entry)
DE	Internalising anti-c-erbB-2 receptor antibody scFv F5.	
XX	Internalising anti-c-erbB-2 receptor antibody scFv F5.	
KW	Antibody; c-erbB-2 receptor; marker; cancer; drug targeting;	
KM	HER/neu oncogene; tumour-specific; internalisation; non-immunogenic.	
OS	Synthetic.	
OS	Homo sapiens.	
XX	Homo sapiens.	
PH	Key	Location/Qualifiers
FT	Region	31..35
FT	Region	/note="Heavy chain variable region (VH) complementarity determining region 1 (CDR1)"
FT	Region	50..66
FT	Region	/note="VH-CDR2"
FT	Region	99..108
FT	Region	/note="VH-CDR3"
FT	Region	157..170
FT	Region	/note="VL-CDR2"
FT	Region	186..192
FT	Region	/note="VL-CDR3"
FT	Region	225..235
FT	Region	/note="VL-CDR3"
XX	MO955367-A1.	
XX	MO955367-A1.	
XX	04-NOV-1999.	
XX	04-NOV-1999.	
XX	23-APR-1999.	99WO-US007395.
XX	23-APR-1999.	99WO-US007395.
XX	24-APR-1998.	98US-0082853P.
XX	24-APR-1998.	98US-0082853P.
XX	12-FEB-1999.	99US-00250056.
XX	12-FEB-1999.	99US-00250056.
XX	(REGC) UNIV CALIFORNIA.	
XX	(REGC) UNIV CALIFORNIA.	
XX	Marke UD, Poul MA;	
XX	Marke UD, Poul MA;	
XX	WPI, 2000-072168/06.	
XX	WPI, 2000-072168/06.	
XX	N-PSDB; AA58235.	
XX	N-PSDB; AA58235.	

PT Novel internalizing antibodies used to treat cancer cells.  
XX  
XX Claim 3; Page 81; 85pp; English.  
XX

CC This sequence represents an internalising humanised antibody, scFv F5, which specifically binds to the extracellular domain of the c-erbB-2 receptor, the protein product of the HER/neu oncogene. The scFv F5 antibody binds to the epitope of the c-erbB-2 receptor that is bound by F5 antibodies. On binding the c-erbB-2 receptor, the antibody is transported into the cell. The c-erbB-2 receptor is a marker protein which is overexpressed by 30-50% of breast carcinomas and other CC adenocarcinomas, and thus provides a useful cell surface marker for specifically targeting tumour cells. The antibodies of the invention are used as tumour-targeting molecules for diagnosis and treatment. The antibodies can be attached to effector molecules. The effector molecules may include cytotoxins such as ricin, abrin or Pseudomonas exotoxin; CC radionuclides; ligands such as growth factors; therapeutic agents such as CC vinylastine, vindesine or melphalan; ribozymes; or antisense molecules. CC The antibodies may also be used for in vivo or in vitro detection and/or CC quantitation of the c-erb-2 receptor and thus diagnosis and/or CC localisation of cancers characterised by expression of c-erb-2. Although CC antibodies have previously been used to target tumour cells, their CC success has been limited. The utility of prior art antibodies has been CC hampered by the paucity of tumour specific antibodies, antibody CC immunogenicity, low binding affinity, and poor tumour penetration. CC Immunogenicity could be avoided and toxicity reduced if high affinity CC tumour specific human antibodies were available. However, the production CC of human monoclonal antibodies using conventional hybridoma technology CC has proven difficult. Also, most of the antibodies produced react with CC antigens that are also common to non-malignant cells, which makes them CC unsuitable for use as tumour-targeting molecules. The antibodies of the CC invention overcome these difficulties, as they are targeted to a tumour- CC specific antigen, and avoid the problem of immunogenicity as they are CC human in origin  
XX

XX Sequence 246 AA:

Query Match 100.0%; Score 1300; DB 3; Length 246;  
Best Local Similarity 100.0%; Pred. No. 3.1e-76;  
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVSGGGLVQPGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSISRGNNTYY 60  
DB 1 QVQLVSGGGLVQPGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSISRGNNTYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYYCAKMTSNAFADYWGQGLTVTVSSG 120  
DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYYCAKMTSNAFADYWGQGLTVTVSSG 120  
QY 121 GGGSGGGSGGGSGSGLVTPPSVSGAPGQRTVISTGSSSNIGAGYGVHWYQQLPGTAP 180  
DB 121 GGGSGGGSGGGSGSGLVTPPSVSGAPGQRTVISTGSSSNIGAGYGVHWYQQLPGTAP 180  
QY 181 KLLIYGNTRPSGVPRFSGFGKTSASLAITGLQADEADYYCCPYDSSLGWFVGGGT 240  
DB 181 KLLIYGNTRPSGVPRFSGFGKTSASLAITGLQADEADYYCCPYDSSLGWFVGGGT 240  
QY 241 KLTVLG 246  
DB 241 KLTVLG 246

RESULT 2

ADN06985  
ID ADN06985 standard; protein; 291 AA.

XX ADN06985;

XX 01-JUL-2004 (first entry)

DE Human EGFR bs-scFv antibody protein, HER3.F4.

XX Bispecific single chain, bs-scFv; cancer;  
KM

KM epidermal growth factor receptor; EGFR; therapy; antibody; human.  
XX  
XX Homo sapiens.  
XX

PN US2004071696-A1.

PD 15-APR-2004.

PF 04-APR-2003; 2003US-00406830.

PR 05-APR-2002; 2002US-0370276P.

PA (REGC) UNIV CALIFORNIA.

PA (FOXC-) FOX CHASE CANCER CENT.

PI Adams GP, Horak EM, Weiner LM, Marks JD;

DR WPI; 2004-328525/30.

PT Novel bispecific antibody comprising first and second antibody joined to each other and having binding specificity to different epitopes of  
PT Epidermal Growth Factor Receptor protein, useful for treating cancer.  
XX

PS Claim 14; SEQ ID NO 2; 57pp; English.

XX The present invention provides bispecific single chain (bs-scFv) antibody CC molecules which may be used to treat various forms of cancer associated CC with the overexpression of the epidermal growth factor receptor (EGFR) CC family. The invention is useful for specifically delivering an effector CC molecule to a cell bearing a receptor from EGFR protein family chosen CC from EGFR, HER2/neu, HER3 and HER4. The invention is useful in the CC treatment of cancer. The present sequence is human EGFR bs-scFv antibody CC protein.  
XX

XX Sequence 291 AA:

Query Match 99.4%; Score 1292; DB 8; Length 291;  
Best Local Similarity 99.6%; Pred. No. 1.2e-75;  
Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVSGGGLVQPGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSISRGNNTYY 60  
DB 23 QVQLVSGGGLVQPGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSISRGNNTYY 82  
QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYYCAKMTSNAFADYWGQGLTVTVSSG 120  
DB 83 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYYCAKMTSNAFADYWGQGLTVTVSSG 142  
QY 121 GGGSGGGSGGGSGSGLVTPPSVSGAPGQRTVISTGSSSNIGAGYGVHWYQQLPGTAP 180  
DB 143 GGGSGGGSGGGSGSGLVTPPSVSGAPGQRTVISTGSSSNIGAGYGVHWYQQLPGTAP 202  
QY 181 KLLIYGNTRPSGVPRFSGFGKTSASLAITGLQADEADYYCCPYDSSLGWFVGGGT 240  
DB 203 KLLIYGNTRPSGVPRFSGFGKTSASLAITGLQADEADYYCCPYDSSLGWFVGGGT 262  
QY 241 KLTVLG 246  
DB 263 KLTVLG 268

RESULT 3

ADN06984  
ID ADN06984 standard; protein; 291 AA.

XX ADN06984;

XX 01-JUL-2004 (first entry)

DE Human EGFR bs-scFv antibody protein, HER3.F4.

XX Bispecific single chain, bs-scFv; cancer;  
KM epidermal growth factor receptor; EGFR; therapy; antibody; human.

XX Homo sapiens.  
 OS US2004071696-A1.  
 XX  
 XX 15-APR-2004.  
 XX  
 XX 04-APR-2003; 2003US-00406830.  
 XX  
 XX 05-APR-2002; 2002US-0370276P.  
 XX  
 XX (REGC ) UNIV CALIFORNIA.  
 XX (FOXC-) FOX CHASE CANCER CENT.  
 XX  
 XX Adams GP, Horak EM, Weiner LM, Marke JD;  
 XX  
 XX WPI; 2004-328525/30.  
 XX  
 XX Novel bispecific antibody comprising first and second antibody joined to  
 PT each other and having binding specificity to different epitopes of  
 PT Epidermal Growth Factor Receptor protein, useful for treating cancer.  
 XX  
 XX Claim 14; SEQ ID NO 1; 57bp; English.  
 XX  
 XX The present invention provides bispecific single chain (bs-scfv) antibody  
 CC molecules which may be used to treat various forms of cancer associated  
 CC with the overexpression of the epidermal growth factor receptor (EGFR)  
 CC family. The invention is useful for specifically delivering an effector  
 CC molecule to a cell bearing a receptor from EGFR protein family chosen  
 CC from EGFR, HER/neu, HER3 and HER4. The invention is useful in the  
 CC treatment of cancer. The present sequence is human EGFR bs-scfv antibody  
 CC protein.  
 XX  
 XX Sequence 291 AA;

Query Match 99.4%; Score 1292; DB 8; Length 291;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-75;  
 Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVSGGGLVOPGSLRLSCAASGFTPRSYAMSVWROAPGKLEWVSAISGRDNTYY 60  
 DB 23 QVQLVSGGGLVOPGSLRLSCAASGFTPRSYAMSVWROAPGKLEWVSAISGRDNTYY 82  
 QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKNTSNAPFDYWGQGLTVTVSSG 120  
 DB 83 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKNTSNAPFDYWGQGLTVTVSSG 142  
 QY 121 GGGSGGGSGGGSGSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYGVHWYQQLPETA 180  
 DB 143 GGGSGGGSGGGSGSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYGVHWYQQLPETA 202  
 QY 181 KLLIYNTNRPSPGVPRFSGFGKSGTSASLAITGLQADEADYYCCQYDSSLSGWVGGGT 240  
 DB 203 KLLIYNTNRPSPGVPRFSGFGKSGTSASLAITGLQADEADYYCCQYDSSLSGWVGGGT 262  
 QY 241 KLTVLG 246  
 DB 263 KLTVLG 268

RESULT 4  
 ADS09297  
 ID ADS09297 standard; protein; 245 AA.

XX ADS09297;  
 XX  
 XX 18-NOV-2004 (first entry)  
 XX  
 XX Human c-Met protein tyrosine kinase antibody, pG1A-4-A12.  
 DE c-Met; tyrosine kinase antibody; antigen binding; cytosolic;  
 XX ophthalmological; antiinflammatory; analgesic; vasodilator; antiproliferative;  
 KW osteoporotic; cancer; tumour; ophthalmic disease; glaucoma; retinitis;

KM retinopathy; uveitis; ocular photophobia; macular degeneration; pain;  
 KM acute injury; eye; hyperproliferative disorder; restenosis; angioplasty;  
 KM psoriasis; HGF; osteoporosis; cancer.  
 XX

OS Homo sapiens.  
 XX  
 XX WO2004072117-A2.  
 XX  
 XX 26-AUG-2004.  
 XX  
 XX 11-FEB-2004; 2004WO-1B000503.  
 XX  
 XX 13-FEB-2003; 2003US-0447073P.  
 XX  
 XX (PHAA ) PHARMACIA CORP.  
 XX  
 XX Morton PA, Arduckle JA, Evans ML, Joy WD, Kahn LE, Shieh JJ;  
 XX  
 XX WPI; 2004-616044/59.  
 XX  
 XX N-PDB; ADS09357.  
 XX

PT Novel c-Met protein tyrosine kinase antibody or its antigen-binding  
 PT portion specifically binding to c-Met, useful for manufacture of  
 PT medicament for treating cancer or tumor and for treatment of ophthalmic  
 PT diseases such as glaucoma.  
 XX  
 XX Claim 1; SEQ ID NO 59; 303bp; English.

XX The invention relates to a novel c-Met protein tyrosine kinase antibody  
 CC or its antigen binding portion that specifically binds to c-Met. The c-  
 CC Met antibody comprises any one of 1-60 fully defined sequence of 238,  
 CC 244, 240, 250, 251, 242, 245, 247, 246, 253, 249, 243, 241, etc., amino  
 CC acids as given in the specification, or its fragment. The invention  
 CC further comprises: a pharmaceutical composition comprising the c-Met  
 CC protein tyrosine kinase antibody and a carrier; an isolated cell that  
 CC produces the c-Met protein tyrosine kinase antibody; and an isolated  
 CC nucleic acid molecule that comprises a nucleic acid sequence that encodes  
 CC a heavy chain or its antigen-binding portion or light chain or its  
 CC antigen-binding portion of the c-Met protein tyrosine kinase antibody.  
 CC The c-Met protein tyrosine kinase antibody has cytostatic,  
 CC ophthalmological, antiinflammatory, analgesic, vasodilator, antiproliferative,  
 CC and osteoporotic activities. The c-Met protein tyrosine kinase antibody is  
 CC useful for the manufacture of medicament for the treatment of cancer or  
 CC tumour. The c-Met protein tyrosine kinase antibody is useful for  
 CC diagnosing the presence or ligation of c-Met expressing tissue. The c-Met  
 CC protein tyrosine kinase antibody is useful for detecting c-Met in a  
 CC biological sample in vitro or in vivo. The c-Met protein tyrosine kinase  
 CC antibody is also useful in the treatment or prevention of ophthalmic  
 CC diseases such as glaucoma, retinitis, retinopathies (e.g., diabetic  
 CC retinopathy), uveitis, ocular photophobia, macular degeneration and pain  
 CC associated with acute injury to the eye. The pharmaceutical composition  
 CC is useful for the treatment of hyperproliferative disorders such as  
 CC restenosis after angioplasty, and psoriasis, and for the treatment of  
 CC animals that lack sufficient HGF, e.g. osteoporosis and cancer. This  
 CC sequence represents the protein of a phage display generated human c-Met  
 CC antibody of the invention.  
 XX  
 XX Sequence 245 AA;

Query Match 87.3%; Score 1135.5; DB 8; Length 245;  
 Best Local Similarity 88.7%; Pred. No. 1.3e-65;  
 Matches 219; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

QY 1 QVQLVSGGGLVOPGSLRLSCAASGFTPRSYAMSVWROAPGKLEWVSAISGRDNTYY 60  
 DB 1 EVQLVESGGGLVAPGSLRLSCAASGFTPRSYAMSVWROAPGKLEWVSAISGRDNTYY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKNTSNAPFDYWGQGLTVTVSSG 120  
 DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADETAVYYCAKNTSNAPFDYWGQGLTVTVSSG 118  
 QY 121 GGGSGGGSGGGSGSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYGVHWYQQLPETA 179

Db	119	GGGGGGGGGGGGGSAQSVLTQPPSVSGARGQRTTISCTGSSSSNIGAGYDVHWQHLPGTA	178
Qy	180	PKLLIYGNTNRPSCGVPDRPFRGKSGTSSASLAITGLQAEADADYYCCFPYSSLSGWFCCG	239
Db	179	PRLLIYGNSNRPSCGVPDRPFRGKSGTSSASLAISGLQAEADADYYCCSYSSLSIDWVFGG	238
Qy	240	TKLTYTIG	246
Db	239	TKVTVLGG	245
RESULT 5			
ADSL12384			
ID	ADSL12384 standard; protein; 251 AA.		
AC	ADSL12384;		
DT	16-DEC-2004 (first entry)		
DE	Human IGF-1R antibody identified as PINT-12A1 Seq 15.		
XX	human; antibody; insulin-like growth factor I receptor; IGF-IR;		
KW	somatomedin-C; cancer; inflammation; pathological liver condition;		
KV	cytostatic; antiinflammatory; hepatotropic; gene therapy.		
XX	Homo sapiens.		
OS	Synthetic.		
PN	WC02004083248-A1.		
PD	30-SEP-2004.		
PF	04-MAR-2004; 2004WO-IB000646.		
PR	14-MAR-2003; 2003US-0455094P.		
PA	(PHAA ) PHARMACIA CORP.		
PI	Morton PA, Arbuckle JA, Bailey KJ, Nicastro PJ, Runnels HA;		
DR	WPI; 2004-691024/67.		
PT	N-PSDB; ADS12403.		
FT	New antibody that specifically binds to insulin-like growth factor I		
PS	receptor for diagnosing or treating cancer, inflammation or pathological		
XX	liver conditions.		
PS	Claim 1; SEQ ID NO 15; 258pp; English.		
XX	This invention relates to a novel antibody or its antigen binding portion		
CC	that binds to the insulin-like growth factor I receptor (IGF-IR), also		
CC	known as somatomedin-C, in order to inhibit binding of IGF-I and IGF-II		
CC	to the receptor (IGF-IR). Specifically, it refers to an IGF-IR antibody		
CC	selected from PINT-6A1, PINT-7A2, PINT-7A4, PINT-7A5, PINT-7A6, PINT-8A1,		
CC	PINT-9A2, PINT-11A1, PINT-11A2, PINT-11A3, PINT-11A4, PINT-11A5, PINT-		
CC	11A7, PINT-11A12, PINT-12A1, PINT-12A2, PINT-12A3, PINT-12A4, and PINT-		
CC	12A5 or fragments thereof. The present invention describes an		
CC	isolated cell line (and non-human transgenic animals) useful for		
CC	expressing nucleic acid molecules that encode at least one variable light		
CC	(VL) and at least one variable heavy (VH) chain antibody regions, as well		
CC	as the pharmaceutical compositions derived thereof. Accordingly, it		
CC	provides a method of diagnosing the presence or location of an IGF-IR-		
CC	expressing tissue, a method for treating diseases such as cancer, as well		
CC	as diagnosing or treating inflammation and other pathological liver		
CC	conditions. As such, these compositions exhibit cytostatic,		
CC	antiinflammatory and hepatotropic activities and can be used for gene		
CC	therapy purposes. The polypeptide sequence is a human IGF-IR antibody		
CC	(seqv) protein of the invention.		
XX	Sequence 251 AA;		
Qy	Query Match	87.1%; Score 1132.5; DB 8; Length 251;	
XX	Beet Local Similarity	86.9%; Pred. No. 2e-65;	

Matches	218:	Conservative	11:	Mismatches	15:	Indels	5:	Gaps	2:
Qy		1	QVQLVESGQGLVOPGSGLRSLCAASGTFPSSYAMSWVRQAPGKGLEWVSALISGRGNTYY	60					
Db		1	EVQLLESGGGGIVPGGSLRLSCAASGTFPSSYAMSWVRQAPGKGLEWVSALISGSGSTYY	60					
Qy		61	ADSVKSGPFTISRDNSKNTLYLQNMSLRAEDTAVYYCAKMT-----SNAFAPDYWGQGLYT	116					
Db		61	ADSVKSGPFTISRDNSKNTLYLQNMSLRAEDTAVYYCARSPVPWADWYFDYDYGKGTMT	120					
Qy		117	VSSSGGGSGGGSGGGSGGS-OSVLTQPPSVSGAPQQRVTISCTGSSSNIIGAGYGVHWQOL	175					
Db		121	VSSSGGGSGGGSGGGSGGSAQAVLTQPPSVSGAPQQRVTISCTGSSRSNFGAGYDVHWQOL	180					
Qy		176	PGTAPKLLIYGNTNRPSPGVDPSPSGFKSGTSSALATIGLQAEDEADYYCCPYDSSLGMY	235					
Db		181	PGTAPKLLIYGNTNRPSPGVDPSPSGSRSGTSASIALTIGLQAEDEADYYCQSYDNLGYSV	240					
Qy		236	FGGGTKYLTIVLG 246						
Db		241	FGGGTKYTVLVG 251						
RESULT 6									
ABP45881		ID	ABP45881	standard; protein; 247 AA.					
XX		AC	ABP45881;						
XX		DT	19-AUG-2002	(first entry)					
XX		DE	Human Blys binding scFv SEQ ID 1892.						
XX		KW	Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;						
KW		KM	tumour necrosis factor; B cell proliferation; B cell differentiation;						
KW		KM	immunosuppressive; immunostimulant; immunomodulatory; antineumatic;						
KM		KM	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;						
KW		KM	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;						
XX		OS	common variable immunodeficiency; acquired immunodeficiency syndrome.						
XX		XX	Homo sapiens.						
XX		XX	WO200202641-A1.						
XX		PD	10-JAN-2002.						
XX		PF	15-JUN-2001; 2001WO-US019110.						
XX		PR	16-JUN-2000; 2000US-0212210P.						
XX		PR	17-OCT-2000; 2000US-0240816P.						
XX		PR	16-MAR-2001; 2001US-0276248P.						
XX		PR	21-MAR-2001; 2001US-0277379P.						
XX		PR	25-MAY-2001; 2001US-0293499P.						
XX		PA	(HUMA-) HUMAN GENOME SCI INC.						
XX		PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.						
XX		PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;						
XX		PI	WPI; 2002-114799/15.						
XX		PT	Antibodies against B lymphocyte Stimulating polypeptides, useful for the						
XX		PT	diagnosis and treatment of cancers and immune disorders.						
XX		PS	Claim 1; Page 2659-2660; 3148bp; English.						
XX		CC	This invention describes novel antibodies that immunospecifically bind to						
CC		CC	B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the						
CC		CC	tumour necrosis factor (TNF) super family and induces B cell						
CC		CC	proliferation and differentiation. The antibodies of the invention have						
CC		CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,						
CC		CC	antineumatic and antiAIDS activity and can be used in vaccines to						
CC		CC	inhibit the expression and activity of Blys. The antibodies bind to Blys						



CC and so may be used to detect and quantitate the presence of BlyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BlyS. They may also be  
 CC administered to treat diseases associated with aberrant BlyS expression  
 CC and actively such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention

XX Sequence 247 AA:

Query Match 86.6%; Score 1125.5; DB 5; Length 247;  
 Best Local Similarity 87.4%; Pred. No. 5,6e-65;  
 Matches 216; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 QVQLVSGGGLVPGGSLRLSCAASGTPRVSVMVWRQAPGKLEWVAISGRGNTYY 60  
 DB 1 QVTLKESGGDLVPGGSLRLSCAASGLTFMSYMTWRQAPGKLEWVAISGSGDNTYY 60  
 QY 61 ADSVKGRTISRDNKNTLYLQNNSLRAEDTAVYYCAKMTSNAPFDYWGQGLTVTVSSG 120  
 DB 61 GDSVGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKMTSNAPFDYWGQGLTVTVSSG 120  
 QY 121 GGGSGGGSGGGGGS-OSVLTQPPSVSGAPGQRTVTSCTGSSSNIGAGYVHWYQQLPGTA 179  
 DB 121 GGGSGGGSGGGGGSASVLTQPPSVSGAPGQRTVTSCTGSSSNIGAGYVHWYQQLPGTA 180  
 QY 180 PKLLIYGNTRPESGVDPRFSGKTSASLAIITGLQAEDEADYYCQPYDSSLGAWPFGG 239  
 DB 181 PRLLISSNTNRPESGVDPRFSGKTSASLAIITGLQAEDEADYYCQPYDSSLGFWFGTG 240  
 QY 240 TKLTVLG 246  
 DB 241 TKVTVLG 247

RESULT 7  
 ADG96708

ID ADG96708 standard; protein; 247 AA.

AC ADG96708;

DT 11-MAR-2004 (first entry)

DE Single chain antibody that immunospecifically binds BlyS SeqID 1892.

XX antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;  
 KW B cell proliferation; differentiation; scfv; myasthenia gravis;  
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;  
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;  
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX Unidentified.

OS Unidentified.

PN MO2003055979-AA2.

PD 10-JUL-2003.

PF 14-NOV-2002; 2002MO-US036496.

PR 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX WPI; 2003-505530/47.

DR Novel antibody that immunospecifically binds to a B lymphocyte stimulator

PT (BlyS), useful for detecting and treating diseases or disorders e.g.

PT rheumatoid arthritis, asthma and leukemia.  
 XX Example 1; SEQ ID NO 1892; 394pp; English.

CC This invention relates to novel antibodies that immunospecifically bind  
 CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to  
 CC chromosome 13q34 and encodes a protein that is a member of the tumour  
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
 CC proliferation and differentiation. Specifically, it refers to single  
 CC chain antibody molecules (scfv) derived, preferably, from the variable  
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
 CC fragment thereof, of either human, murine, rat or monkey BlyS. The  
 CC present invention refers to the use of such antibodies in various methods  
 CC for the detection, diagnosis and prognosis of diseases related to the  
 CC aberrant expression or inappropriate function of BlyS or its receptor. As  
 CC such, these compositions are useful for identifying immune disorders  
 CC including myasthenia gravis and multiple sclerosis, inflammatory  
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
 CC lymphoma. Accordingly, they can be described as exhibiting various  
 CC activities such as antirheumatic, antiallergic and cytoprotective,  
 CC antiinflammatory, antiasthmatic, antiallergic and cytoprotective. This  
 CC polypeptide sequence is a single chain antibody that binds BlyS of the  
 CC invention. NOTE: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format  
 CC directly from WIP0 at ftp.wipo.int/pub/published pct\_sequences.

XX Sequence 247 AA:

Query Match 86.6%; Score 1125.5; DB 7; Length 247;  
 Best Local Similarity 87.4%; Pred. No. 5,6e-65;  
 Matches 216; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 QVQLVSGGGLVPGGSLRLSCAASGTPRVSVMVWRQAPGKLEWVAISGRGNTYY 60  
 DB 1 QVTLKESGGDLVPGGSLRLSCAASGLTFMSYMTWRQAPGKLEWVAISGSGDNTYY 60  
 QY 61 ADSVKGRTISRDNKNTLYLQNNSLRAEDTAVYYCAKMTSNAPFDYWGQGLTVTVSSG 120  
 DB 61 GDSVGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKMTSNAPFDYWGQGLTVTVSSG 120  
 QY 121 GGGSGGGSGGGGGS-OSVLTQPPSVSGAPGQRTVTSCTGSSSNIGAGYVHWYQQLPGTA 179  
 DB 121 GGGSGGGSGGGGGSASVLTQPPSVSGAPGQRTVTSCTGSSSNIGAGYVHWYQQLPGTA 180  
 QY 180 PKLLIYGNTRPESGVDPRFSGKTSASLAIITGLQAEDEADYYCQPYDSSLGAWPFGG 239  
 DB 181 PRLLISSNTNRPESGVDPRFSGKTSASLAIITGLQAEDEADYYCQPYDSSLGFWFGTG 240  
 QY 240 TKLTVLG 246  
 DB 241 TKVTVLG 247

RESULT 8  
 ADS92884

ID ADS92884 standard; protein; 258 AA.

AC ADS92884;

DT 02-DEC-2004 (first entry)

DE Human Myo28 antibody single chain Fv fragment (scfv) germlined protein.

XX Human; Myo28; single chain Fv fragment; scfv;

XX growth and differentiation factor-8; GDF-8;

XX bone morphogenetic protein-11; BMP-11; muscle strength; muscle mass;

XX ActRIIB; muscle repair; glucose tolerance; neuromuscular disorder;

XX bone degenerative disorder; muscular dystrophy;

XX Duchenne muscular dystrophy; muscular atrophy; organ atrophy;

XX carpal tunnel syndrome; congestive obstructive pulmonary disease;

XX cachexia; muscle wasting syndrome; amyotrophic lateral sclerosis;

XX obesity; adipose tissue disorder; syndrome X; impaired glucose tolerance;



DB 181 ABKLLIYGTTPSPGVDRFSGSGKSTASLAITGLQAEADYFCQSDSSLSGVSFG 240

QY 239 GTRKLTVLG 246

DB 241 GTRKLTVLG 248

RESULT 10

ABP45967

ID ABP45967 standard; protein; 247 AA.

AC ABP45967;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scfv seq ID 1978.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KM common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

OS

PN MO200202641-A1.

XX 10-JAN-2002.

PD

XX 15-JUN-2001; 2001WO-US019110.

PF

XX 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 2760-2761; 3148pp; English.

XX

XX This invention describes novel antibodies that immunospecifically bind to

CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of Blys. The antibodies bind to Blys

CC and so may be used to detect and quantitate the presence of Blys in

CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of Blys. They may also be

CC administered to treat diseases associated with aberrant Blys expression

CC and activity such as cancer, immune, and autoimmune disorders and

CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,

CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and

CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

CC the antibodies and fragments of the antibodies described in the method of

CC the invention

XX

XX Sequence 247 AA;

XX

Query Match 85.7%; Score 1113.5; DB 5; Length 247;

Best Local Similarity 85.8%; Pred. No. 3,4e-64;

Matches 212; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTPRSYAMSVRQAPGKLEWVSALISGRGDNTRY 60

DB 1 EVQLVETGGGLVQPGGSLRLSCAASGLTFTSSIAMTWVRQAPGKLEWVSALISGNSNTTH 60

QY 61 ADSVKGRFTTISRDNKNTLYLQMNSLRAEDTAVYTCARNTSNAPFDYQGQTLVTVSSG 120

DB 61 ADFVKGKRFPTASRDNKSLIYLQMNSLTADDSAVYCAKNGFYREYMGQGLTLVTVSSG 120

QY 121 GGGSGGGSGGGGGS-QSVLTQPPSVGARGQVLTISCTSSSSNIGAGYGVHWYQQLPRTA 179

DB 121 GGGSGGGSGGGGSAQSVLTQPPSVGARGQVLTISCTSSSSNIGAGYGVHWYQQLPRTA 180

QY 180 PKLLIYGNTRNRPSPGVDRFSGSGKSTASLAITGLQAEADYFCQSDSSLSGVSFGG 239

DB 181 PKLLIFGNNNRPSGVDRFSGSGKSTASLAITGLQPDDEADYFCQSDSSLSGVSFGG 240

QY 240 TKLTVLG 246

DB 241 TKLTVLG 247

RESULT 11

ADG96794

ID ADG96794 standard; protein; 247 AA.

XX

AC ADG96794;

XX

DT 11-MAR-2004 (first entry)

DE

XX Single chain antibody that immunospecifically binds Blys seqid 1978.

XX

KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;

KW B cell proliferation; differentiation; scfv; myasthenia gravis;

KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;

KW carcinoma; lymphoma; antirheumatic; antirheumatic; neuroprotective;

KW antiinflammatory; antiaesthetic; antiasthergic; cytostatic.

XX

OS Unidentified.

XX

PN WO2003055979-A2.

XX

PD 10-JUL-2003.

XX

PF 14-NOV-2002; 2002WO-US036496.

PR 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX WPI; 2003-505530/47.

XX

PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator

PT (Blys), useful for detecting and treating diseases or disorders e.g.

PT rheumatoid arthritis, asthma and leukemia.

XX

XX Example 1; SEQ ID NO 1978; 394pp; English.

XX

XX This invention relates to novel antibodies that immunospecifically bind

CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to

CC chromosome 13q34 and encodes a protein that is a member of the tumour

CC necrosis factor superfamily and induces both in vivo and in vitro B cell

CC proliferation and differentiation. Specifically, it refers to single

CC chain antibody molecules (scfvs) derived, preferably, from the variable

CC heavy CDR3 region that immunospecifically bind to a polypeptide, or

CC fragment thereof, of either human, murine, rat or monkey Blys. The

CC present invention refers to the use of such antibodies in various methods

CC for the detection, diagnosis and prognosis of diseases related to the

CC aberrant expression or inappropriate function of Blys or its receptor. As

CC such, these compositions are useful for identifying immune disorders





OY 240 TKLTVLG 246  
 DB 241 TKLTVLG 247

## RESULT 15

ID ADG96769 standard; protein; 247 AA.

AC ADG96769;

DT 11-MAR-2004 (first entry)

DE Single chain antibody that immunospecifically binds Blys segid 1953.

XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;  
 KW B cell proliferation; differentiation; scfv; myasthenia gravis;  
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;  
 KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;  
 KW antinflammatory; antiaesthetic; antiallergic; cytostatic.

OS Unidentified.

PN WO2003055979-A2.

PD 10-JUL-2003.

PF 14-NOV-2002; 2002WO-US036496.

PR 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

DR WPI; 2003-505530/47.

PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
 PT (Blys), useful for detecting and treating diseases or disorders e.g.  
 PT rheumatoid arthritis, asthma and leukemia.

PS Example 1; SEQ ID NO 1953; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind  
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to  
 CC chromosome 13q34 and encodes a protein that is a member of the tumour  
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
 CC proliferation and differentiation. Specifically, it refers to single  
 CC chain antibody molecules (scfvs) derived, preferably, from the variable  
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
 CC fragment thereof, of either human, murine, rat or monkey Blys. The  
 CC present invention refers to the use of such antibodies in various methods  
 CC for the detection, diagnosis and prognosis of diseases related to the  
 CC aberrant expression or inappropriate function of Blys or its receptor. As  
 CC such, these compositions are useful for identifying immune disorders  
 CC including myasthenia gravis and multiple sclerosis, inflammatory  
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
 CC as AIDS and proliferative disorders including leukemia, carcinoma and  
 CC lymphoma. Accordingly, they can be described as exhibiting various  
 CC activities such as antirheumatic, antiallergic, neuroprotective,  
 CC antinflammatory, antiaesthetic, antiallergic and cytostatic. This  
 CC polypeptide sequence is a single chain antibody that binds Blys of the  
 CC invention. NOTE: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published pct\_sequences.

XX Sequence 247 AA;

Query Match 84.0%; Score 1092.5; DB 7; Length 247;  
 Best Local Similarity 85.8%; Pred. No. 7.6e-63;  
 Matches 212; Conservative 10; Mismatches 24; Indels 1; Gaps 1;

OY 1 QVQLVSGGGLVQPGSRLRLSCAAGFTFRSYAMSVNRQAPGKLEWVSALISGRDNTYY 60  
 DB 1 EVQLVESGGGLVQPGMSLRSLCAAGFTFRYSAMTWVRQAPGKLEWVSALITSSGATYY 60  
 OY 61 ADSVKGRTFTSRDNRKNTLYLQMSLRADPTAVVYCAKRTSNAFAPDVGQGTLLTVSSG 120  
 DB 61 ADSVKGRTFTSRDNRKNTLYLQMSLRADPTAVVYCAKRTGNGYFPDVGQGTLLTVSSG 120  
 OY 121 GGGSGGGSGGGGS-QSVLTQPPSVSGAPGQRVTISCTGSSNIGAGYGVHWYQQLPGTA 179  
 DB 121 GGGSGGGSGGGGSASQSVLTQPPSVSGAPGQRVTISCTGRSSNIGAGFPVHWYQLPGTA 180  
 OY 180 PKLLIYGNTNRPSGVPPDRFSGKSGTSASLAITGLQAEDEADYYCQFYDSSLGWFVGGG 239  
 DB 181 PKVLIYGNRNRPSSGVPPDRFSGKSGTSASLAITGLQAEDEADYYCQSYDRSLRAEFVGTG 240  
 OY 240 TKLTVLG 246  
 DB 241 TKLTVLG 247

Search completed: April 19, 2005, 16:39:11  
 Job time : 123.992 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2005, 16:32:47 ; Search time 30.2459 seconds  
(without alignments)  
607.146 Million cell updates/sec

Title: US-09-250-056B-1

Perfect score: 1300  
Sequence: 1 QVQLVSGGGLVQPGGSLRLT...YDSISLGWVGGGTTLTVLG 246

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/prodata/1/1aa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1075.5	82.7	310	3	US-09-079-029-11 Sequence 11, App1
2	1017.5	78.3	334	4	US-09-046-028-53 Sequence 53, App1
3	1017.5	78.3	339	4	US-09-046-028-55 Sequence 55, App1
4	1017.5	78.3	348	4	US-09-046-028-51 Sequence 51, App1
5	892.5	68.7	312	3	US-09-079-029-10 Sequence 10, App1
6	887	68.2	358	2	US-09-079-029-9 Sequence 9, App1
7	883.5	68.0	258	2	US-08-665-202-5 Sequence 5, App1
8	883.5	68.0	258	4	US-09-315-574-5 Sequence 5, App1
9	855	65.8	240	4	US-09-192-854-2 Sequence 2, App1
10	852.5	65.6	280	3	US-09-260-527-1 Sequence 1, App1
11	841.5	64.7	281	3	US-09-025-769B-178 Sequence 178, App
12	841.5	64.7	281	4	US-09-490-070A-178 Sequence 178, App
13	841.5	64.7	281	4	US-09-490-153-178 Sequence 178, App
14	841.5	64.7	281	4	US-09-490-324-178 Sequence 178, App
15	827	63.6	268	4	US-09-976-118-1 Sequence 1, App1
16	819.5	63.0	245	4	US-08-918-148-75 Sequence 75, App1
17	819.5	63.0	245	4	US-09-138-091A-73 Sequence 73, App1
18	794.5	61.1	245	4	US-08-918-148-78 Sequence 78, App1
19	793.5	61.0	245	4	US-09-138-091A-76 Sequence 76, App1
20	792.5	61.0	245	3	US-08-918-148-76 Sequence 76, App1
21	792.5	61.0	245	4	US-09-138-091A-74 Sequence 74, App1
22	791.5	60.9	249	3	US-08-918-148-74 Sequence 74, App1
23	791.5	60.9	249	4	US-09-138-091A-72 Sequence 72, App1
24	781	60.1	244	3	US-08-918-148-77 Sequence 77, App1
25	781	60.1	244	4	US-09-138-091A-75 Sequence 75, App1
26	768	59.1	236	4	US-08-190-199A-65 Sequence 65, App1
27	768	59.1	244	3	US-08-918-148-79 Sequence 79, App1

28	768	59.1	244	4	US-09-138-091A-77 Sequence 77, App1
29	765	58.8	301	2	US-08-661-052-14 Sequence 14, App1
30	765	58.8	301	3	US-09-188-082-14 Sequence 14, App1
31	765	58.8	301	3	US-09-364-088-14 Sequence 14, App1
32	765	58.8	301	3	US-09-102-716-14 Sequence 14, App1
33	765	58.8	553	2	US-08-661-052-16 Sequence 16, App1
34	765	58.8	553	3	US-09-188-082-16 Sequence 16, App1
35	765	58.8	553	3	US-09-364-088-16 Sequence 16, App1
36	765	58.8	553	3	US-09-102-716-16 Sequence 16, App1
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41	740.5	57.0	240	1	US-08-477-484B-148 Sequence 148, App
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44	740.5	57.0	240	3	US-09-136-389-148 Sequence 148, App
45	740.5	57.0	240	3	US-09-610-838-148 Sequence 148, App

ALIGNMENTS

RESULT 1  
US-09-079-029-11  
; Sequence 11, Application US/09079029  
; Patent No. 6342369  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camilia W.  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Chuntarapai, Anan  
; APPLICANT: Kim, Kyung J.  
; TITLE OF INVENTION: Apo-2 Receptor  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,029  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/952-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 310 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-09-079-029-11  
Query Match 82.7%; Score 1075.5; DB 3; Length 310;  
Best Local Similarity 84.6%; Pred. No. 3.7e-75;  
Matches 208; Conservative 11; Mismatches 26; Indels 1; Gaps 1;  
QY 1 QVQLVSGGGLVQPGGSLRLTSCAAGFTFRSYAMVRAQPKGLAEWVAISGRGDNITY 60  
DB 40 QVQLVSGGGLVQPGGSLRLTSCAAGFTFRSYAMVRAQPKGLAEWVAISGRGDNITY 99  
QY 61 ADVKGRFTISRDNKNTLYIQMNSLRADETAVYCAKKTNAFAFDYWGQGLTVTVSSG 120















Db :||| |||:||||  
237 PYVFGTKVIVIG 250

Search completed: April 19, 2005, 16:45:19  
Job time : 31.2459 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: April 19, 2005, 16:43:24 ; Search time 88.7213 Seconds  
(without alignments)  
921.573 Million cell updates/sec

Title: US-09-250-056b-1

Perfect score: 1300  
Sequence: 1 QVQLVESGGGLVQPGGSLRL.....YDSLSGWFVGGTKLTVLG 246

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep.\*  
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16: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubppaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1300	100.0	246	17	US-10-855-755-1
2	1292	99.4	291	15	US-10-406-830-1
3	1292	99.4	291	15	US-10-406-830-2
4	1135.5	87.3	245	16	US-10-779-461-59
5	1125.5	86.6	247	10	US-09-880-748-1892
6	1125.5	86.6	247	15	US-10-293-418-1992
7	1121.5	86.3	258	16	US-10-688-925-20
8	1113.5	85.7	247	10	US-09-880-748-1978
9	1113.5	85.7	247	15	US-10-293-418-1978
10	1096.5	84.3	258	16	US-10-688-925-8
11	1092.5	84.0	247	10	US-09-880-748-1953
12	1092.5	84.0	247	15	US-10-293-418-1953
13	1092	84.0	252	10	US-09-880-748-1519

14	1092	84.0	252	15	US-10-293-418-1519	Sequence 1519, Ap
15	1084	83.4	258	16	US-10-779-461-1	Sequence 1, Appl
16	1081	83.2	252	10	US-09-880-748-1362	Sequence 1362, Ap
17	1081	83.2	252	15	US-10-293-418-1362	Sequence 1362, Ap
18	1080	83.1	258	10	US-09-880-748-1841	Sequence 1841, Ap
19	1080	83.1	258	15	US-10-293-418-1841	Sequence 1841, Ap
20	1076.5	82.8	243	10	US-09-880-748-1969	Sequence 1969, Ap
21	1076.5	82.8	243	15	US-10-293-418-1969	Sequence 1969, Ap
22	1075.5	82.7	310	13	US-10-052-798-11	Sequence 11, Appl
23	1075.5	82.7	310	14	US-10-286-917-11	Sequence 11, Appl
24	1075.5	82.7	310	15	US-10-423-448-11	Sequence 11, Appl
25	1069	82.2	252	10	US-09-880-748-1201	Sequence 1201, Ap
26	1069	82.2	252	15	US-10-293-418-1201	Sequence 1201, Ap
27	1065.5	82.0	262	16	US-10-688-925-2	Sequence 2, Appl
28	1062	81.7	250	10	US-09-880-748-1420	Sequence 1420, Ap
29	1062	81.7	250	15	US-10-293-418-1420	Sequence 1420, Ap
30	1059.5	81.5	253	14	US-10-120-414-76	Sequence 76, Appl
31	1056	81.2	246	14	US-10-120-414-80	Sequence 80, Appl
32	1053.5	81.0	243	16	US-10-779-461-46	Sequence 46, Appl
33	1048	80.6	250	10	US-09-880-748-1461	Sequence 1461, Ap
34	1048	80.6	250	15	US-10-293-418-1461	Sequence 1461, Ap
35	1045	80.4	246	16	US-10-779-461-45	Sequence 45, Appl
36	1045	80.4	246	16	US-10-779-461-47	Sequence 47, Appl
37	1044.5	80.3	245	16	US-10-779-461-24	Sequence 24, Appl
38	1044	80.3	248	10	US-09-880-748-1890	Sequence 1890, Ap
39	1044	80.3	248	15	US-10-293-418-1890	Sequence 1890, Ap
40	1043	80.2	240	10	US-09-880-748-1905	Sequence 1905, Ap
41	1043	80.2	240	15	US-10-293-418-1905	Sequence 1905, Ap
42	1040.5	80.0	243	14	US-10-322-673-51	Sequence 51, Appl
43	1039	79.9	240	10	US-09-880-748-2016	Sequence 2016, Ap
44	1039	79.9	240	15	US-10-293-418-2016	Sequence 2016, Ap
45	1039	79.9	260	10	US-09-880-748-1458	Sequence 1458, Ap

## ALIGNMENTS

RESULT 1  
US-10-855-755-1  
; Sequence 1, Application US/10855755  
; Publication No. US20050037339A1  
; GENERAL INFORMATION:  
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
; APPLICANT: Marke, James D  
; APPLICANT: Poul, Marie A  
; APPLICANT: Becerril, Balazar  
; TITLE OF INVENTION: METHODS OF SELECTING INTERNALIZING ANTIBODIES  
; FILE REFERENCE: 4070-895011US  
; CURRENT APPLICATION NUMBER: US/10/855,755  
; CURRENT FILING DATE: 2004-05-26  
; PRIOR APPLICATION NUMBER: US 60/082,953  
; PRIOR FILING DATE: 1998-04-24  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 246  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Human phage display antibody  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (31)..(35)  
; OTHER INFORMATION: VH-CDR1  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (50)..(66)  
; OTHER INFORMATION: VH-CDR2  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (99)..(108)  
; OTHER INFORMATION: VH-CDR3  
; FEATURE:

NAME/KEY: SITE  
LOCATION: (157)..(170)  
OTHER INFORMATION: VL-CDR1  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (186)..(192)  
OTHER INFORMATION: VL-CDR2  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (225)..(235)  
OTHER INFORMATION: VL-CDR3  
US-10-855-755-1

Query Match 100.0%; Score 1300; DB 17; Length 246;  
Best Local Similarity 100.0%; Pred. No. 7.8e-81;  
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQVSEGGGLVQPGSLRLSCAAGFTFRSYAMSWRQAPGKLEWVAISGRGNTYY 60  
DB 1 QVQVSEGGGLVQPGSLRLSCAAGFTFRSYAMSWRQAPGKLEWVAISGRGNTYY 60  
QY 61 ADVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKMTSNAFAFDYWGQGLTVTVSSG 120  
DB 61 ADVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKMTSNAFAFDYWGQGLTVTVSSG 120  
QY 121 GGGSGGGSGGGSGSOSVLTQPPSVSGAPGQRTVISTGSSSNIGAGYVHWYQQLPGTAP 180  
DB 121 GGGSGGGSGGGSGSOSVLTQPPSVSGAPGQRTVISTGSSSNIGAGYVHWYQQLPGTAP 180  
QY 181 KLLIYGNTRPSGVDRFSGFGKSGTSASLAITGLQAEDEADYCCQFYDSSLGWFVGGGT 240  
DB 181 KLLIYGNTRPSGVDRFSGFGKSGTSASLAITGLQAEDEADYCCQFYDSSLGWFVGGGT 240  
QY 241 KLTVLG 246  
DB 241 KLTVLG 246

## RESULT 2

US-10-406-830-1  
Sequence 1, Application US/10406830  
Publication No. US20040071696A1  
GENERAL INFORMATION:  
APPLICANT: ADAMS, GREGORY P.  
APPLICANT: HORAK, EVA M.  
APPLICANT: WEINER, LOUIS M.  
APPLICANT: JAMES, MARKS D.  
TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: 407T-000410US  
CURRENT APPLICATION NUMBER: US/10/406,830  
CURRENT FILING DATE: 2003-04-04  
PRIOR APPLICATION NUMBER: US 60/370,276  
PRIOR FILING DATE: 2002-04-05  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1  
LENGTH: 291  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic antibody.  
US-10-406-830-1

Query Match 99.4%; Score 1292; DB 15; Length 291;  
Best Local Similarity 99.6%; Pred. No. 3.2e-80;  
Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQVSEGGGLVQPGSLRLSCAAGFTFRSYAMSWRQAPGKLEWVAISGRGNTYY 60  
DB 23 QVQVSEGGGLVQPGSLRLSCAAGFTFRSYAMSWRQAPGKLEWVAISGRGNTYY 82  
QY 61 ADVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKMTSNAFAFDYWGQGLTVTVSSG 120

DB 83 ADVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKMTSNAFAFDYWGQGLTVTVSSG 142  
QY 121 GGGSGGGSGGGSGSOSVLTQPPSVSGAPGQRTVISTGSSSNIGAGYVHWYQQLPGTAP 180  
DB 143 GGGSGGGSGGGSGSOSVLTQPPSVSGAPGQRTVISTGSSSNIGAGYVHWYQQLPGTAP 202  
QY 181 KLLIYGNTRPSGVDRFSGFGKSGTSASLAITGLQAEDEADYCCQFYDSSLGWFVGGGT 240  
DB 203 KLLIYGNTRPSGVDRFSGFGKSGTSASLAITGLQAEDEADYCCQFYDSSLGWFVGGGT 262  
QY 241 KLTVLG 246  
DB 263 KLTVLG 268

## RESULT 3

US-10-406-830-2  
Sequence 2, Application US/10406830  
Publication No. US20040071696A1  
GENERAL INFORMATION:  
APPLICANT: ADAMS, GREGORY P.  
APPLICANT: HORAK, EVA M.  
APPLICANT: WEINER, LOUIS M.  
APPLICANT: JAMES, MARKS D.  
TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: 407T-000410US  
CURRENT APPLICATION NUMBER: US/10/406,830  
CURRENT FILING DATE: 2003-04-04  
PRIOR APPLICATION NUMBER: US 60/370,276  
PRIOR FILING DATE: 2002-04-05  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2  
LENGTH: 291  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic antibody.  
US-10-406-830-2

Query Match 99.4%; Score 1292; DB 15; Length 291;  
Best Local Similarity 99.6%; Pred. No. 3.2e-80;  
Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQVSEGGGLVQPGSLRLSCAAGFTFRSYAMSWRQAPGKLEWVAISGRGNTYY 60  
DB 23 QVQVSEGGGLVQPGSLRLSCAAGFTFRSYAMSWRQAPGKLEWVAISGRGNTYY 82  
QY 61 ADVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKMTSNAFAFDYWGQGLTVTVSSG 120  
DB 83 ADVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKMTSNAFAFDYWGQGLTVTVSSG 142  
QY 121 GGGSGGGSGGGSGSOSVLTQPPSVSGAPGQRTVISTGSSSNIGAGYVHWYQQLPGTAP 180  
DB 143 GGGSGGGSGGGSGSOSVLTQPPSVSGAPGQRTVISTGSSSNIGAGYVHWYQQLPGTAP 202  
QY 181 KLLIYGNTRPSGVDRFSGFGKSGTSASLAITGLQAEDEADYCCQFYDSSLGWFVGGGT 240  
DB 203 KLLIYGNTRPSGVDRFSGFGKSGTSASLAITGLQAEDEADYCCQFYDSSLGWFVGGGT 262  
QY 241 KLTVLG 246  
DB 263 KLTVLG 268

## RESULT 4

US-10-779-461-59  
Sequence 59, Application US/10779461  
Publication No. US20040166544A1  
GENERAL INFORMATION:  
APPLICANT: Morton, Philip A



Db 181 PRLISSNTNRPSGVDPD



RESULT 11  
US-09-880-748-1953  
Sequence 1953, Application US/09880748  
Publication No. US20030059937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PFS3  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16

Query Match	84.0%	Score 1092.5	DB 15	Length 247
Best Local Similarity	85.8%	Pred. No. 9	9e-67	
Matches 212	Conservative 10	Mismatches 24	Indels 1	Gaps 1

[illegible]

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RESULT 13
US-09-880-748-1519
; Sequence 1519, Application US/09880748
; Publication No. US20030059937A1
GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyss
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver..2.0
; SEQ ID NO 1519
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1519

```

Query Match	84.0%	Score 1092;	DB 10;	Length 252;
Best Local Similarity	84.5%	Pred. No. 1,1e-66;		
Matches	213;	Conservative	9;	Mismatches 24; Indels 6; Gaps 2

  

QY	1	QVQLVESGGGLVPGGSLRLSCAAGGFTTRKATAMGWKRAQPKGLEWVAISAGRDNTYY	60
Db	1	QVQLVESGGGVVQPRSLRLSCAAGGFTTSSGMMHWRAQPKGLEWVAISYDSNKYY	60
QY	61	ADSVKGRFTISPDNSKNTLYLQMNSLRADTAVYYCAK-----MTSNAPAFPDYGGGTLV	115
Db	61	ADSVKGRFTISPDNSKNTLYLQMNSLRADTAVYYCAKQYDILTCYGGPFYWGGMV	120
QY	116	TYSGGGGSGGGGGSGGGGSS-QSVLTROPPEVSQAQPGQVITISCTGSSSNTGAGYGVHWYQQ	174
Db	121	TYSGGGGSGGGGGSGGGGSAQAQVLTROPSSVSQAQPGQVSVSGTGSSSNTGAGDVHWYQQ	180
QY	175	LPGTAPKLLIYGNTRPSPGVPDFSGFKGTASALAITLQAEDEADYYCOFEDSSLSGM	234
Db	181	FPGTAPKLLIYGNNNRPSPGVPRFVSXGTSALAITLQAEDEADYYCOGVDSSLSST	240
QY	235	VFGGTKLTVLG	246
Db	241	IFGTGKTVLG	252

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RESULT 14
US-10-293-418-1519
? Sequence 1519, Application US/10293418
? Publication No. US20030223956A1
? GENERAL INFORMATION:
? APPLICANT: Ruben et al.
? TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
? FILE REFERENCE: PFS23P2
? CURRENT APPLICATION NUMBER: US/10/293,418
? CURRENT FILING DATE: 2002-11-27
? PRIOR APPLICATION NUMBER: 60/331,469
? PRIOR FILING DATE: 2001-11-16
? PRIOR APPLICATION NUMBER: 60/340,817
? PRIOR FILING DATE: 2001-12-19
? PRIOR APPLICATION NUMBER: 09/880,748
? PRIOR FILING DATE: 2001-06-15
? PRIOR APPLICATION NUMBER: 60/293,499
? PRIOR FILING DATE: 2001-05-25
? PRIOR APPLICATION NUMBER: 60/277,379
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/276,248
? PRIOR FILING DATE: 2001-03-16
? PRIOR APPLICATION NUMBER: 60/240,816
? PRIOR FILING DATE: 2000-10-17
? PRIOR APPLICATION NUMBER: 60/212,210
? PRIOR FILING DATE: 2000-06-16
? NUMBER OF SEQ ID NOS: 3247
? SEQ ID NO 1519
? LENGTH: 252
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-293-418-1519

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```

Query Match          84.0%; Score 1092; DB 15; Length 252;
Best Local Similarity 84.5%; Pred. No. 1,1e-66;
Matches 213; Conservative 9; Mismatches 24; Indels 6; Gaps 2

DB      1  QVVLVESGGGLVDPGSGLRLLSCAASGFPTFRSYAMSWYQAPGKGLMEVSAISGRDNTYY 60
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1  QVQLQESGGGVQPPQSRSLRLSCAASGFTFSISYGMHWYQAPGKGLMEVAIVSYDSNKTY 60
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

DB      61  ADSVKGRTTISRDNKNTLYLQMSLRADETAIVVYCAR----MTSNAFAPDYWGQTLV 115
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      61  ADSVKGRTTISRDNKNTLYLQMSLRADETAIVVYCARQYDILTGYGGFDYWGQTLV 120
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

DB      116  TVSSGGGGSGGGSGGGSGGS--QSVLTQPPSVSGAPGQRYTISTGSSSNIGAGYGVHWIQ 174
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      121  TVSSGGGGSGGGSGGGSGGAQAVLTQPPASVSGAPGQRYSVSCTGSSSNIGAGYDVHWYQQ 180
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

DB      175  LPGAHPKLLIIGNTRPESGVDPDRFSGFGSGHSALATIGLQAEDEADYVCCQYDSSLSGM 234
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      181  PPGTAPKLLIIGNNNRPESGVDPDRFVSXGTSASLAITGLQAEDEADYVCCQYDSSLSGT 240
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

DB      235  VEGGGTKLTVLG 246
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      241  IFGTGKTVLIG 252
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-10-779-461-1
; Sequence 1, Application US/10779461
; Publication No. US20040166544A1
; GENERAL INFORMATION:
; APPLICANT: Morton, Philip A
; TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS
; FILE REFERENCE: 00980/1
; CURRENT APPLICATION NUMBER: US/10/779,461
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/447,073
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 161

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SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1  
LENGTH: 238  
TYPE: PRT  
ORGANISM: artificial  
FEATURE:  
OTHER INFORMATION: phage display generated human antibody  
US-10-779-461-1

Query Match 83.4%; Score 1084; DB 16; Length 238;  
Best Local Similarity 86.6%; Pred. No. 3.6e-66;  
Matches 214; Conservative 7; Mismatches 14; Indels 12; Gaps 3;

Qy	1	QVQLVESGGGLVQP	GGSLRLSCAASGFTFRSYAMSWVRQAPGKLEWVS	AI	SGRDNTYY	60
Db	1	EVQLLESGRGLVQPG	SLRLSCAASGFTFSYAMSWVRQAPGKLEWVS	AI	SGSGSTYY	60
Qy	61	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCAR		120
Db	61	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCAR		110
Qy	121	GGSGGGSGGGSGGS	-OSVLTQPPSVSGAPGQRTISCTGSSSNIGAGYGVHWYQQL	PGTA		179
Db	111	GGSGGGSGGGSGGS	AAQAVLTQPSVS	GAPGQRTISCTGSSSNIGADYDHWYQQL	PGTA	170
Qy	180	PKLLIYGNTNRPSG	VPDRFSGFKGT	SASLAITGLQAEDEADYYCQFYDSLSGM	-VFGG	238
Db	171	PKLLIYGNNRPSG	VDPRFSGSKGT	SASLAITGLQAEDEADYYCQSYDNSPDAYVVF	FGG	230
Qy	239	GTKLTIVL				245
Db	231	GTKLTIVL				237

Search completed: April 19, 2005, 17:00:52  
Job time : 90.7213 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using SW model

Run on: April 19, 2005, 16:32:07 ; Search time 27.7254 Seconds  
(without alignments)  
853.705 Million cell updates/sec

Title: US-09-250-056B-1

Sequence: 1 QVQLVSGGGLVQPGGSLRL.....YDSLSGMVFGGKTLTVLG 246

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	612	47.1	268	2 A56446	Ig heavy chain V r
2	611.5	47.0	249	2 S41374	single chain Fv an
3	556	42.8	119	2 S31107	Ig heavy chain - h
4	554.5	42.7	233	2 JCS322	p53 specific singl
5	548	42.2	119	2 C36005	Ig heavy chain V r
6	546	42.0	119	2 S31108	Ig heavy chain - h
7	545.5	42.0	111	2 S36274	Ig lambda chain V
8	542	41.7	140	2 S31588	Ig heavy chain V r
9	541	41.6	138	2 S31666	Ig heavy chain V r
10	540	41.5	140	2 S31686	Ig heavy chain V r
11	540	41.5	119	2 D36005	Ig heavy chain V r
12	540	41.5	123	2 S31114	Ig heavy chain - h
13	539	41.5	127	2 S38489	Ig heavy chain - h
14	538.5	41.4	124	2 S20782	Ig heavy chain V r
15	537	41.3	112	2 S51148	antibody light cha
16	531.5	40.9	120	2 S48798	Ig heavy chain V r
17	529	40.7	160	2 S05271	Ig heavy chain pre
18	526	40.5	121	2 I55673	Ig heavy chain - h
19	523	40.2	135	2 S31598	Ig heavy chain V r
20	521	40.1	236	2 S25746	Ig lambda chain -
21	520	40.0	134	2 S31699	Ig heavy chain V r
22	513	39.5	119	2 F36005	Ig heavy chain V r
23	512	39.4	120	2 S36278	Ig heavy chain V r
24	511.5	39.3	140	2 S70442	Ig heavy chain pre
25	510.5	39.3	112	2 P31447	Ig heavy chain V r
26	508	39.1	121	2 S19666	Ig heavy chain V r
27	508	39.1	121	2 G36005	Ig heavy chain V r
28	507.5	39.0	133	2 S31510	Ig heavy chain - h
29	507	39.0	109	2 P31649	Ig heavy chain V r

30	507	39.0	132	2 S31603	Ig heavy chain V r
31	507	39.0	134	2 S31679	Ig heavy chain V r
32	504.5	38.8	216	2 S29258	Ig lambda chain V
33	503.5	38.7	120	2 S31112	Ig heavy chain - h
34	502.5	38.7	114	2 S31120	Ig heavy chain - h
35	502.5	38.7	118	2 S31116	Ig heavy chain - h
36	502.5	38.7	120	2 S44111	Ig heavy chain pre
37	502.5	38.7	151	2 A60943	Ig heavy chain V-D
38	502	38.6	121	2 S31113	Ig heavy chain - h
39	502	38.6	125	2 S30531	Ig heavy chain V r
40	501.5	38.6	143	2 S23624	Ig heavy chain V r
41	501	38.5	217	2 U60246	Ig lambda chain NI
42	500.5	38.5	114	2 S46390	Ig heavy chain V r
43	500.5	38.5	122	2 S31117	Ig heavy chain V r
44	499.5	38.4	108	2 P31648	Ig heavy chain V r
45	498.5	38.3	137	2 S31701	Ig heavy chain V r

## ALIGNMENTS

## RESULT 1

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Jan-1996 #sequence #revision 19-Jan-1996 #text\_change 16-Aug-1996  
C/Accession: A56446  
R/Tang, P.M.; Poltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident

A/Reference number: A56446; MUID:95229583; PMID:7713873  
A/Accession: A56446  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-268 <TRAN>  
A/Cross-references: GB:U20617  
C/Keywords: heterotrimer; immunoglobulin

Query Match  
Best Local Similarity 51.2%; Pred. No. 8.2e-34;  
Matches 126; Conservative 35; Mismatches 75; Indels 10; Gaps 5;

QY	1 QVQLVSGGGLVQPGGSLRLSCAASGFTPRSYAMSWRQAPKGLIEWVAISRGDNITY 60	47.1%; Score 612; DB 2; Length 268;
DB	3 QVQLVSGGGLVQPGGSLRLSCAASGFTPRSYAMSWRQAPKGLIEWVAISRGDNITY 62	
QY	61 ADSVKGRFTISRDNSKNTLYIQMNSLRADTVVYCAKMTSNAPFDYGGGTLTVSSG 120	
DB	63 DKPFGKATIAADTSNTAVYQLSSITSEDIIVYVCASYLTRYE-NYMGCGTTVVS 121	
QY	121 GGGSGGGSGGGSGGSSVLTQPPSV--SGAPGQRVTISCTGSSS--NIGAGYGVHMYOQLPCT 178	
DB	122 GGGSGGGSGGGSGGSDIELTQSPALMSASLGEVYVMSCRASSVNF-----ITWYQKSDA 176	
QY	179 APKLIVYGNTPRPSGVDPDRFGSKGTSASLAITQLADEADYVCOFYDSSLSGMVFGG 238	
DB	177 SKLWVYVYSHLPQGVPAFSSGSGSGMSYSLTSSMEGDATVYCOQRTS--SPTFSS 234	
QY	239 GTKLTIV 244	
DB	235 GTKLTIV 240	

## RESULT 2

S41374  
single chain Fv antibody - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence #revision 06-Jan-1995 #text\_change 06-Jan-1995  
C/Accession: S41374  
R/Artezenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.  
Submitted to the EMBL Data Library, January 1994  
A/Description: Construction and functional characterization of a single chain Fv antibod

A:Accession: S41374  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-249 <ART>  
 A:Cross-references: EMBL:Z29480

Query Match 47.0%; Score 611.5; DB 2; Length 249;  
 Best Local Similarity 52.6%; Pred. No. 8.3e-34;  
 Matches 130; Conservative 34; Mismatches 74; Indels 9; Gaps 5;

QY 1 QVQLVSSGGLVQPGGSLRLSCAASGFTPRSYAMSWVRQAPGKLEWVSALISGRDNTYY 60  
 DB 1 QVQLQOSGAEIVRFEGASVSLCTASGFNKRDIYHWKQRPKGLMIRIAPASGNVYK 60  
 QY 61 ADSVKGRTISRDNKNTLYLQWNSLRADDTAVYYCAKMTSNAPAFDYWGQGLTVTVSS 120  
 DB 61 VRFPODKATITADTSNTAVYLLSLTSBDAVYVCARDTLVYLSGVWGQGSTVTVSSR 120  
 QY 121 GGGSGGGSGGGSGSVLTQ-PPSVSGAQQQRTVITCTGSSNT---GAGYGVHWYQQLP 176  
 DB 121 GGGSGGGSGGGSGDIELTQSPSVVAVIPGESVVISCRSSKSLVSDGDSY-LFWFLQRP 179  
 QY 177 GPAPKLLIYGNTRPSPGVPDRPSGFGSKTSASLAITGLQAEDEADYYC-QFYDSSLSGWV 235  
 DB 180 GGSFOLLIRMSNLASGVDFDRPSGSGSTISFTLRISVAEDVGYTCMQHREYPLT--- 236  
 QY 236 FGGGTXTL 242  
 DB 237 FGA GTXTL 243

## RESULT 3

Ig heavy chain - human  
 S31107  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
 C:Accession: S31107  
 R:Raaphorst, F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
 Eur. J. Immunol. 22, 247-251, 1992  
 A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem  
 A:Reference number: S31104; MUID:92111633; PMID:1730252  
 A:Accession: S31107  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <RNA>  
 A:Cross-references: EMBL:X62955  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 42.8%; Score 556; DB 2; Length 119;  
 Best Local Similarity 89.9%; Pred. No. 1.9e-30;  
 Matches 107; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLVSSGGLVQPGGSLRLSCAASGFTPRSYAMSWVRQAPGKLEWVSALISGRDNTYY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKLEWVSALISGSGSTYY 60  
 QY 61 ADSVKGRTISRDNKNTLYLQWNSLRADDTAVYYCAKMTSNAPAFDYWGQGLTVTVSS 119  
 DB 61 ADSVKGRTISRDNKNTLYLQWNSLRADDTAVYYCAKDPGASGYFDYWGQGLTVTVSS 119

## RESULT 4

p53 specific single-chain antibody Pab421 - human  
 JCS322  
 C:Species: Homo sapiens (man)  
 C:Date: 15-May-1997 #sequence\_revision 15-May-1997 #text\_change 18-Jul-1997  
 C:Accession: JCS322  
 R:Janot, C.B.; Hynes, N.E.  
 Biochem. Biophys. Res. Commun. 230, 242-246, 1997  
 A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.

A:Reference number: JCS322; MUID:97168950; PMID:9016757  
 A:Accession: JCS322  
 A:Molecule type: mRNA  
 A:Residues: 1-233 <JAN>  
 A:Experimental source: hybridoma cell  
 C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 42.7%; Score 554.5; DB 2; Length 233;  
 Best Local Similarity 50.6%; Pred. No. 4.7e-30;  
 Matches 122; Conservative 25; Mismatches 83; Indels 11; Gaps 5;

QY 6 EGGGGLVQPGGSLRLSCAASGFTPRSYAMSWVRQAPGKLEWVSALISGRDNTYYADSVK 65  
 DB 2 EGGGGLVQPGGSLRLSCAASGFTPRSYAMSWVRQAPGKLEWVSALISGRDNTYYADSVK 61  
 QY 66 GRFTISRDNKNTLYLQWNSLRADDTAVYYCAKMTSNAPAFDYWGQGLTVTVSSGGGSG 125  
 DB 62 VAKITMTADTSSNTAVLQSLSLTSBDAVYVC-----NA-GMDYWGQGLTVTVSSGGGSG 115  
 QY 126 GGGSGGGSGSVLTQ-PPSVSGAQQQRTVITCTGSSNTGAGYG-VHWYQQLPRTAPKLL 183  
 DB 116 GRASGGGGSDIELTQSPASLAVSLQQRATISCRASKSVTSQSYMHMNOQRPGPRL 175  
 QY 184 IYGNTRPSPGVPDRPSGFGSKTSASLAITGLQAEDEADYYCQFYDSSLSGWFGGXTLT 243  
 DB 176 IYVSNLSGVPARPSGSGSDFTLNHPVEEDATYYCOHIRELTRS---EGGTXLE 232  
 QY 244 V 244  
 DB 233 I 233

## RESULT 5

Ig heavy chain V region (30p1) - human  
 C36005  
 C:Species: Homo sapiens (man)  
 C:Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Aug-1996  
 C:Accession: C36005  
 R:Schroeder Jr., H.W.; Wang, J.Y.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
 A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
 A:Reference number: A36005; MUID:90349571; PMID:2117273  
 A:Accession: C36005  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <SCH>  
 A:Cross-references: GB:M18513  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 42.2%; Score 548; DB 2; Length 119;  
 Best Local Similarity 89.1%; Pred. No. 6.5e-30;  
 Matches 106; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLVSSGGLVQPGGSLRLSCAASGFTPRSYAMSWVRQAPGKLEWVSALISGRDNTYY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKLEWVSALISGSGSTYY 60  
 QY 61 ADSVKGRTISRDNKNTLYLQWNSLRADDTAVYYCAKMTSNAPAFDYWGQGLTVTVSS 119  
 DB 61 ADSVKGRTISRDNKNTLYLQWNSLRADDTAVYYCAKDPGASGYFDYWGQGLTVTVSS 119

## RESULT 6

Ig heavy chain - human  
 S31108  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
 C:Accession: S31108  
 R:Raaphorst, F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
 Eur. J. Immunol. 22, 247-251, 1992  
 A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem



A:Reference number: S31104; MUID:92111633; PMID:1730252  
 A:Accession: S31108  
 A:Status: Preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <RNA>  
 A:Cross-references: EMBL:X62956  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 42.0%; Score 546; DB 2; Length 119;  
 Best Local Similarity 89.1%; Pred. No. 8.8e-30;  
 Matches 106; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSAISGRGNTYY 60  
 DB 1 EVQLLESGGGLVQPGGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSAISGGSTYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKMTSNAPFDYWGQTLVTYSS 119  
 DB 61 ADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKMDRLTGTDFYWGQTLVTYSS 119

RESULT 7  
 S36274  
 Ig lambda chain V region (clone alpha-THY-32) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
 C:Accession: S36274  
 R:Griffiths, A.D.; Malnig-Vale, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.  
 EMBL J. 12, 725-734, 1993

A:Title: Human anti-self antibodies with high specificity from phage display libraries.  
 A:Reference number: S36256; MUID:93178448; PMID:7679990  
 A:Accession: S36274  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-111 <GR1>  
 A:Cross-references: EMBL:Z18835; NID:G33420; PIDN:CAA79287.1; PID:933913  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 42.0%; Score 545.5; DB 2; Length 111;  
 Best Local Similarity 93.8%; Pred. No. 8.9e-30;  
 Matches 105; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 135 QSVLTQPPSVSGAPGQRTVITSGSSSNIGAGYGVHMYQQLPCTAPKLLIYGNTNPPSGV 194  
 DB 1 QSVLTQPPSVSGAPGQRTVITSGTSSNIGAGYGVHMYQQLPCTAPKLLIYGNSNPPSGV 59

QY 195 PPRFSGKSGTSLAITGLQADEADYYQFPDSSLSGVRFGGTRKLTVLG 246  
 DB 60 PPRFSGKSGTSLAITGLQADEADYYCQSYDSSLSGVRFGGTRKLTVLG 111

RESULT 8  
 S31588  
 Ig heavy chain V region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S31588  
 R:Cuisinier, A.M.; Gauthier, L.; Boudli, L.; Fougereau, M.; Tonnelle, C.  
 submitted to the EMBL Data Library, June 1992  
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A:Reference number: S31585  
 A:Accession: S31588  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-140 <CUI>

A:Cross-references: EMBL:Z14200; NID:G30957; PIDN:CAA78569.1; PID:930958  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 41.7%; Score 542; DB 2; Length 140;  
 Best Local Similarity 88.4%; Pred. No. 1.9e-29;  
 Matches 107; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSAISGRGNTYY 60  
 DB 20 EVQLLESGGGLVQPGGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSAISGGSTYY 79

QY 61 ADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAK--MTSNAPFDYWGQTLVTYSS 118  
 DB 80 ADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKHDSNYTYFDYWGQTLVTYSS 139

QY 119 S 119  
 DB 140 S 140

RESULT 9  
 S31666  
 Ig heavy chain V region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S31666  
 R:Cuisinier, A.M.; Gauthier, L.; Boudli, L.; Fougereau, M.; Tonnelle, C.  
 submitted to the EMBL Data Library, June 1992  
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A:Reference number: S31585  
 A:Accession: S31666  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-138 <CUI>

A:Cross-references: EMBL:Z14202; NID:G30963; PIDN:CAA78571.1; PID:930964  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 41.6%; Score 541; DB 2; Length 138;  
 Best Local Similarity 87.4%; Pred. No. 2.2e-29;  
 Matches 104; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSAISGRGNTYY 60  
 DB 20 EVQLLESGGGLVQPGGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSAISGGSTYY 79

QY 61 ADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKMTSNAPFDYWGQTLVTYSS 119  
 DB 80 ADSVKGRFTISRDNKNTLYLQNNSLRAEDTAVYYCAKARTGYWYFDLWGRGTLVTYSS 138

RESULT 10  
 S31686  
 Ig heavy chain V region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C:Accession: S31686  
 R:Cuisinier, A.M.; Gauthier, L.; Boudli, L.; Fougereau, M.; Tonnelle, C.  
 submitted to the EMBL Data Library, June 1992  
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A:Reference number: S31585  
 A:Accession: S31686  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-140 <CUI>

A:Cross-references: EMBL:Z14205; NID:G30969; PIDN:CAA78574.1; PID:930970  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 41.6%; Score 541; DB 2; Length 140;  
 Best Local Similarity 86.8%; Pred. No. 2.2e-29;  
 Matches 105; Conservative 6; Mismatches 8; Indels 2; Gaps 1;

A:Reference number: S31104; MUID:92111633; PMID:1730252  
 A:Accession: S31108  
 A:Status: Preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-119 <RNA>  
 A:Cross-references: EMBL:X62956  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

QY 1 QVQLVSGGSLVNPGGSLILSCAASGFTERYAMWVQAPEKGLIEWSAISGRGDMTTY 60  
 Db 20 EVQLLESGGSLVPPGGSLLRSCAASGFTSSYAMWVQAPEKGLIEWSAISGSGSSTYY 79  
 QY 61 ADSVKGRFTISRDNSKNTLYLQWNSLRAEETAVYYCAK--MTSNAFAFDYWGCGELTVTS 118  
 Db 80 SDSVKGRFTISRDNSKNTLYLQWNSLRAEETAVYYCAKCPFAGSPSPFDYWGCGELTVTS 139  
 QY 119 S 119  
 Db 140 S 140

## RESULT 11

Ig heavy chain V region (M43) - human  
CSpecies: Homo sapiens (man)  
CDate: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #ext\_change 16-Dec-1998  
CAccession: D36005  
R:Schroeder Jr., H.W., Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A>Title: Preferential utilization of conserved immunoglobulin heavy chain variable genes  
A:Reference number: A36005; MUID:90349571; PMID:211773  
A:Accession: D36005  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-119 <SCH>  
A:Cross-references: GB:M34024  
C:Genetics:  
A:Gene: GDB:IGH@; IGHV1  
A:Cross-references: GDB:118731; OMIM:146910  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F15-98/Domain: immunoglobulin homology <IMV>

Query Match	41.5%	Score 540;	DB 2;	Length 119;
Best Local Similarity	89.1%;	Pred. No. 2.2e-29;		
Matches 106; Conservative	3;	Mismatches 10;	Indels 0;	Gaps 0

[illegible]

## RESULT 12

Ig heavy chain human  
C:Species: Homo sapiens (man)  
C:Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C:Accession: S31114  
R:Rapoport, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Voessen, J.M.; Schuurman  
Bur, J. Immunol. 22, 247-251, 1992  
A>Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement  
A:Reference number: S31104; MUID:92111633; PMID:1730252  
A:Accession: S31114  
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-123 <RNA>  
A:Cross-references: EMBL:X62963  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
C:15-98/Domain: immunoglobulin homology <IM>

Query Match	41.5%	Score 540;	DB 2;	Length 123;
Best Local Similarity	86.2%;	Pred. No. 2.3e-29;		
Matches 106; Conservative	5;	Mismatches 8;	Indels 4;	Gaps 1

Qy	1	QVQVLSGGGLVQPGGSLRLSCAAGFTRSYAMSWQAQFGKGLIEWSAISGRDNTYY	60
	:		
	:		
	:		
Db	1	EVLLSSGGGLVQPGGSLRLSCAAGFTFSSYAMSWQAQFGKGLIEWSAISGGGSSITY	60
Qy	61	ADSVKGRFTTISRDNKNTLYLQMSLRAEDTAVYYCAK---MTSNAPAPDYGQGLVLT	114
	:		
	:		
	:		
Db	61	ADSVKGRFTTISRDNKNTLYLQMSLRAEDTAVYYCAQASLYLRFLEMLFDYMGQGLVLT	120
Qy			
	117	VSS	119
Db			
	121	VSS	123

## RESULT 13

Ig heavy chain human (fragment)  
 C|Species: Homo sapiens (man)  
 C|Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
 J|Accession: S38489  
 R|Marks, J.D.; Overhand, W.H.; Bye, J.M.; Finnean, R.; Gorick, B.D.; Voak, D.; Thorpe, S.  
 submitted to the EMBL Data Library, June 1993  
 A|Description: Human antibody fragments specific for human blood group antigens from a p  
 A|Reference number: S38488  
 A|Accession: S38489  
 A|Status: preliminary  
 A|Molecule type: DNA  
 A|Residues: 1-127 <MAR>  
 A|Cross-references: EMBL:Z23028; NID:G414025; PIDN:CAA80563.1; PID:G414026  
 C|Superfamily: immunoglobulin V region; immunoglobulin homology  
 C|Keywords: heterotetramer; immunoglobulin  
 F|15-98/Domain: immunoglobulin homology<IMM>

Query Match	41.5%	Score 539;	DB 2;	Length 127;
Best Local Similarity	82.7%;	Pred. No. 2.7e-29;		
Matches 105; Conservative	6;	Mismatches 6;	Indels 10;	Gaps 1

QY QVLTIVSSGGGLVPGGSLTLCASAGFTFRSTAMSMWRQAGKGLIEWASLSAGGADTTY 60  
Db QVLTIVSSGGGLVPGGSLTLCASAGFTFRSTAMSMWRQAGKGLIEWASLSAGGADTTY 60  
QY QVLTIVSSGGGLVPGGSLTLCASAGFTFRSTAMSMWRQAGKGLIEWASLSAGGADTTY 60  
Db QVLTIVSSGGGLVPGGSLTLCASAGFTFRSTAMSMWRQAGKGLIEWASLSAGGADTTY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRADPTAVYCAM-----TSMAFPIYNG 110  
Db 61 ADSVKGRFTISRDNKNTLYLQMSLRADPTAVYCAEGEPASDYYDSGGYISFPYNG 120

Qy	111	QGTLETV	117
Db	121	QGTLETV	127

## RESULT 14

Ig heavy chain V region - human  
C/Species: Homo sapiens (man)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C/Accession: S20782  
R/Mortari, F.; Wang, J.; Schroeder, H.W.  
submitted to the EMBL Data Library, April 1992  
A/Description: Analysis of the IGA and IGG rearranged VH repertoire of human cord blood  
A/Reference number: S20765  
A/Accession: S20782  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-124 <MOR>  
A/Cross-references: EMBL:Z11946; NID:q33897; PIDN:CAA78003.1; PID:g33898  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match	41.4%;	Score 538.5;	DB 2;	length 124;
Best Local Similarity	84.7%;	Pred. No. 2.9e-29;		
Matches 105; Conservative	5;	Mismatches 9;	Indels 5;	Gaps 1

```
QY      1 QVQLVESGGGLVQPGGSLRLSCASGFTFRSYAMSWVROAPGKLEWVSAISGRGNTYY 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 EVQLLESGGGLVQPGGSLRLSCASGFTFRSYAMSWVROAPGKLEWVSTISGSGDSTYY 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 ADSVNGRFTISRDNKNTLYLQNNSLRADPTAVYYCARMTSNFA-----FDYWGQGLV 115
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 ADSVNGRFTISRDNKNTLYLQNNSLRADPTAVYYCAKRIALFGVVIPIPHFDYWGQGLV 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      116 TVSS 119
      :|||:
Db      121 TVSS 124
```

## RESULT 15

```
S51148
antibody light chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S51148
R:de Krulif, J.; Boel, E.; Logtenberg, T.
submitted to the EMBL Data Library, January 1995
A:Description: Selection and application of human SCFV antibody fragments from a semi-sy
A:Reference number: S51147
A:Accession: S51148
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <DEK>
A:Cross-references: UNIPROT:Q8WUK4; EMBL:X83713
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:13-90/Domain: immunoglobulin homology <IMM>
```

```
Query Match      41.3%; Score 537; DB 2; Length 112;
Best Local Similarity 94.5%; Pred. No. 3.3e-29;
Matches 103; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      138 LTQPPSVSGAPGQRTVISTCTGSSSNIGAGIGVHWYQQLPGTAPKLIYGNTRRPSGVPR 197
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      2 LTQPPSVSGAPGQRTVISTCTGSSSNIGAGIGVHWYQQLPGTAPKLIYGNTRRPSGVPR 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      198 FSGFKSGTASLAIITGLQABDEADYCCOPYDSLSGWFVGGGTKLTVLG 246
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      62 FSGSKSGTASLAIITGLQABDEADYCCOSYDSLSGSAFPGGTKLTVLG 110
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

Search completed: April 19, 2005, 16:44:12  
Job time : 28.7254 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2005, 16:24:02 ; Search time 118.967 Seconds

(without alignments)  
1058.876 Million cell updates/sec

Title: US-09-250-056B-1

Perfect score: 1300

Sequence: 1 QVQLVSGGGLVPGGSLRL.....YDSLSGWFVGGGTLTVLG 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1613378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1613378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	803	61.8	240	2 Q65ZC9	Q65ZC9 homo sapien
2	771	59.3	255	2 Q6XB05	Q6XB05 mus musculu
3	707.5	54.4	248	2 Q65ZG7	Q65ZG7 mus sp. b3(
4	685.5	52.7	298	2 Q9QYF0	Q9QYF0 synthetic C
5	641	49.3	244	2 Q65ZC8	Q65ZC8 homo sapien
6	593	45.6	243	2 Q7TQM2	Q7TQM2 mus musculu
7	592	45.5	241	2 Q921A6	Q921A6 mus musculu
8	587	45.2	487	2 Q65ZL2	Q65ZL2 mus sp. fv/
9	553	42.5	236	2 Q6GMX4	Q6GMX4 homo sapien
10	535	41.2	257	2 Q96BB9	Q96BB9 homo sapien
11	527.5	40.6	218	2 Q925S1	Q925S1 mus musculu
12	523	40.2	236	2 Q6GMX3	Q6GMX3 homo sapien
13	518	39.8	236	2 Q96B61	Q96B61 homo sapien
14	517.5	39.8	613	2 Q8WUX1	Q8WUX1 homo sapien
15	505	38.8	121	2 Q9UL71	Q9UL71 homo sapien
16	502.5	38.7	464	2 Q6MZU6	Q6MZU6 homo sapien
17	498	38.3	113	2 Q9UL90	Q9UL90 homo sapien
18	492.5	37.9	118	2 Q9UL91	Q9UL91 homo sapien
19	491.5	37.8	122	1 HV3G_HUMAN	P01768 homo sapien
20	491	37.8	116	2 Q9ULJ3	Q9ULJ3 homo sapien
21	489.5	37.7	473	2 Q6MZV7	Q6MZV7 homo sapien
22	488.5	37.6	475	2 Q6MZQ6	Q6MZQ6 homo sapien
23	488	37.5	470	2 Q6PUD4	Q6PUD4 homo sapien
24	486	37.4	494	2 Q96K68	Q96K68 homo sapien
25	486	37.3	478	2 Q6PI81	Q6PI81 homo sapien
26	484.5	36.9	606	2 Q6GMV2	Q6GMV2 homo sapien
27	479.5	36.9	112	2 Q9HCC1	Q9HCC1 homo sapien
28	479.5	36.9	118	2 Q9UL72	Q9UL72 homo sapien
29	476	36.6	117	1 HV3C_HUMAN	P01764 homo sapien
30	476	36.6	573	2 Q8WJ38	Q8WJ38 homo sapien
31	474	36.5	115	1 HV3D_HUMAN	P01765 homo sapien

32	473.5	36.4	122	2 Q9UL84	Q9UL84 homo sapien
33	473	36.4	121	1 HV3J_HUMAN	P01771 homo sapien
34	472.5	36.3	130	1 LVIG_HUMAN	P06316 homo sapien
35	471.5	36.3	147	2 Q9Y509	Q9Y509 homo sapien
36	471	36.2	472	2 Q6N089	Q6N089 homo sapien
37	469	36.1	119	1 HV3I_HUMAN	P01770 homo sapien
38	467.5	36.0	493	2 Q6GMX2	Q6GMX2 homo sapien
39	463.5	35.7	2	Q99KA4	Q99KA4 mus musculu
40	462.5	35.6	122	1 HV3H_HUMAN	P01769 homo sapien
41	462	35.5	119	2 Q920E7	Q920E7 mus musculu
42	460.5	35.4	465	2 Q6PEC4	Q6PEC4 homo sapien
43	459.5	35.3	122	1 HV3A_HUMAN	P01762 homo sapien
44	456.5	35.1	235	2 Q6GMW6	Q6GMW6 homo sapien
45	456	35.1	473	2 Q91205	Q91205 mus musculu

## ALIGNMENTS

## RESULT 1

Q65ZC9 PRELIMINARY; PRT; 240 AA.

AC Q65ZC9; 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, last annotation update)  
DE Single-chain Fv (Fragment).  
GN Name=scFv;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Clq/7; PubMed:9219263;  
RX MEDLINE=97362799; PubMed:9219263;  
RA Kontermann R.E., Wing M.G., Winter G.;  
RT "Complement recruitment using bispecific diabodies.";  
RL Nat. Biotechnol. 15:629-631(1997).  
DR EMBL: Y13056; CAA73499.1; -  
DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003596; IG\_v.  
DR Pfam: PF00047; IG\_2.  
DR SMART: SM00409; IG\_2.  
DR SMART: SM00406; IG\_2.  
DR PROSITE: PS50835; IG-LIKE; 2.  
FT NON\_TER 1  
FT NON\_TER 240  
SQ SEQUENCE 240 AA; 25569 MW; FDCPD3645F64B373 CRC64;

Query Match 61.8%; Score 803; DB 2; Length 240;

Best Local Similarity 68.2%; Pred. No. 1,1e-48; Mismatches 167; Conservative 17; Mismatches 53; Indels 8; Gaps 4;

QY	1	QVQLVSGGGLVPGGSLRLSCAASGFTPRSYAMSWRQAPGKLEWVAISRGCHNTYY	60
DB	1	QVQLVSGGGLVPGGSLRLSCAASGFTPRSYAMSWRQAPGKLEWVAISRGCHNTYY	60
QY	61	ADSVKRFITSRDNTLTLYLQNSLRADTAVYCAKRTSNFAFDYWGQGLTVTVSSG	120
DB	61	ADSVKRFITSRDNTLTLYLQNSLRADTAVYCAKRTSNFAFDYWGQGLTVTVSSG	120
QY	121	GGSGGGGGGGGGGGGSLVLPPE-VGAGAGQRTTICTGSSNIGAGYGVHWYQQLPGR	179
DB	119	GGSGGGGGGGGGGGGSLVLPPE-VGAGAGQRTTICTGSSNIGAGYGVHWYQQLPGR	175
QY	180	PKLLIYGNTRPESGVDPFGSGTSASIAITGLQADEADYCYCOFYDSSLGWFVGGG	239
DB	176	PKLLIYKASSIASRAFRSGSGGTDFTLTISLPDPDPATYTCQY--SNPLPFGGG	233
QY	240	TKLTV 244	

Db 234 TKLEI 238

RESULT 2

06KB05 PRELIMINARY; PRT; 255 AA.

AC 06KB05

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DE SCFV B8E5 protein (Fragment).

GN Name=SCFV B8E5.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Balb/c;

RA Briand J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ746180; CAG34081.1; -.

DR HSSP; P01837; 1KCR.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_V.

DR SMART; SM00409; IG; 2.

DR SMART; SM00406; IG; 2.

DR PROSITE; PSS0835; IG\_LIKE; 2.

FT NON\_TER 1

SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 59.3%; Score 771; DB 2; Length 255;

Best Local Similarity 62.5%; Pred. No. 2, 1e-46;

Matches 157; Conservative 31; Mismatches 53; Indels 10; Gaps 6;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWRQAPGKLEWVSATSGRDNTYY 60

DB 1 QVQLQSGGDLVKGPGSLKVSCAASGFTFSYGMWVRQTPDKLEWVAITISGGSYTY 60

QY 61 ADSVGRFTISRDNKNTLYLQMSLRADDAVYCAKMTSNAF--AFYWGQGLTVTVS 118

DB 61 PSVVGKRFITSRDNKNTLYLQMSLRADDAVYCAKMTSNAF--AFYWGQGLTVTVS 120

QY 119 SGSGSGSGSGSGSGSGSVLTQ--PPEVSGAPGQRTISCTGSSSNIGA---GYGVHWYQ 173

DB 121 SGSGSGSGSGSGSGSGSDIYMAQSPSLYSAGEKVTMSCKSSQSLNSKQKMY-LAWYQ 179

QY 174 QLEPTAKLLIYGNTRPSGVDPDRPSGKSGTSASIAITGLQAEDEADYVCFYDSSLG 233

DB 180 QKPGQSPKLLIYGASRRESGVDPDRFTGSGSGTDFTLTISVQAEADLAIVYCC-NHDSYP- 237

QY 234 WYFGGSGTKLV 244

DB 238 LTFGAGTKLEI 248

RESULT 3

06S207 PRELIMINARY; PRT; 248 AA.

AC 06S207

DT 25-OCT-2004 (TREMBlrel. 28, Created)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DE B3 (Fv)-PE40 (Fragment).

GN Name=B3 (Fv)-PE40;

OS Mus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10095;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92020904; PubMed=1924323;

RA Brinkmann U., Pai L.H., Fitzgerald D.J., Williamson M., Pastan I.,

RT "B3 (Fv)-PE38KDEL, a single-chain immunotoxin that causes complete

RT regression of a human carcinoma in mice."

RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620 (1991).

DR EMBL; S57990; AAB1971.2; -.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_V.

DR Pfam; PF00047; IG; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00406; IG; 2.

DR PROSITE; PSS0835; IG\_LIKE; 2.

FT NON\_TER 248

SQ SEQUENCE 248 AA; 26634 MW; 7A359BA3E570950 CRC64;

Query Match 54.4%; Score 707.5; DB 2; Length 248;

Best Local Similarity 59.7%; Pred. No. 5, 8e-42;

Matches 148; Conservative 30; Mismatches 61; Indels 9; Gaps 5;

QY 2 VOLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWRQAPGKLEWVSATSGRDNTYYA 61

DB 3 VLVESGGGLVQPGGSLKLSAATSGFTISDYMYWVRQTPDKLEWVAISNDSSAAYS 62

QY 62 DSVKGRFTISRDNKNTLYLQMSLRADDAVYCAKMTSNAFAPDWGQGLTVTVSSG 121

DB 63 DTVKGRFTISRDNKNTLYLQMSLRADDAVYCAKMTSNAFAPDWGQGLTVTVSSG 122

QY 122 GSGSGSGSGSGSGSVLTQPP--SVSGAPGQRTISCTGSS---SNIGAGVHWYQQLP 176

DB 123 GSGSGSGSGSGSGSVLTQSPSLPSVSGDQSLTSCRSQITVHSH-GNTY-LHWYQQLP 180

QY 177 GAPKLLIYGNTRPSGVDPDRPSGKSGTSASIAITGLQAEDEADYVCFYDSSLGWF 236

DB 181 GQSPKLLIYKYSNRSVGPDRPSGSGSGTDFTLKISRVEADLGVYCC--FGSHVPTFF 238

QY 237 GGGTYLV 244

DB 239 GSGTKLEI 246

RESULT 4

09QYF0 PRELIMINARY; PRT; 298 AA.

AC 09QYF0

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE CN 8 single chain antibody.

GN Name=CN 8 scFv;

OS synthetic construct.

OC other sequences; artificial sequences.

OX NCBI\_TaxID=32630;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20183931; PubMed=10706631; DOI=10.1073/pnas.050582197;

RA Shinohara N., Demura T., Fukuda H.,

RT "Isolation of a vascular cell wall-specific monoclonal antibody

RT recognizing a cell polarity by using a phage display subtraction

RT method."

RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).

DR EMBL; AB036341; BAA88633.1; -.

DR PIR; A33933; A33933.

DR PIR; S19112; S19112.

DR HSSP; P01820; 1A70.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_V.

DR SMART; SM00406; IG; 2.

DR PROSITE; PSS0835; IG\_LIKE; 2.

SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 52.7%; Score 685.5; DB 2; Length 298;

Best Local Similarity 56.2%; Pred. No. 2, 4e-40;

Matches	140;	Conservative	30;	Mismatches	64;	Indels	15;	Gaps	5;
Qy		1	QVQLVESGGGLVQPGGSLRLSCAASGFTFRYSAMSWVQAPRGKGLEWYSAISGRDNTYY	60					
Db		40	QVRLQDSGGGLVYKPPGSGLTKSCAASGSPFSRYSMSWVQAPOKGLIEWIGEINPDSTINY	99					
Qy		61	ADSVKGRFTISRDNSKNTLYIQOMNSLRADFTAVVYCAK--MTSNAPAFDPYWGQGLTVYSSG	120					
Db		100	TPSLDKRTIISRDNAKNTLYIQOMSVRSADTALYCAAPSYGHS-AYMGQGTIVYVSSG	158					
Qy		121	GGSGGGGGGGGGSGQSVLTQ--PPSYGAPGQKRVITISCTGSSSNIGAGYGVH---WYQL	175					
Db		159	GGSGGGGGGGGGSGSDIELTQSPASISASVGEIVTITCCASGN-----IHNYLAWYQOK	211					
Qy		176	PETAPKLLIYGNTRPSPGVDPDFSGFSGKTSASLAITGLQAEDEADYICQFYDSSLGCV	235					
Db		212	QKGSFQLLYVNAKTLADGVPSRFSGSGSGGTQYSLKINSIQPEDFSGSYCCQHWL--TPT	269					
Qy		236	FGGGTKLTV	244					
Db		270	FGGGTKLEI	278					
RESULT 5									
Q65ZC8		Q65ZC8	PRELIMINARY;	PRT;	244	AA.			
AC		Q65ZC8;							
DT		25-OCT-2004 (TREMBLrel. 28, Created)							
DT		25-OCT-2004 (TREMBLrel. 28, Last sequence update)							
DT		25-OCT-2004 (TREMBLrel. 28, Last annotation update)							
DE		Single-chain Fv (Fragment).							
GN		Name=ecfv;							
OS		Homo sapiens (Human).							
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC		Mammalia; Euteria; Primates; Carnivora; Homidae; Homo.							
NCBI		Taxid=9606;							
RP		[1]							
RP		SEQUENCE FROM N.A.							
RX		MEDLINE=97362799; PubMed=9219263;							
RA		Kontermann R.E., Wing M.G., Winter G.;							
RT		"Complement recruitment using bispecific diabolies.";							
RL		Nat. Biotechnol. 15:629-631(1997).							
DR		EMBL, Y13057; CAA73500.1; -.							
DR		InterPro; IPR003599; IG.							
DR		InterPro; IPR007110; IG_1like.							
DR		InterPro; IPR003596; IG_v.							
DR		Pfam; PF00047; Ig_2.							
DR		SMART; SM00409; IG_2.							
DR		SMART; SM00406; IGV_2.							
DR		PROSITE; PS50835; IG_LIKE; 2.							
DR		NON_TER	1						
FT		NON_TER	1						
FT		SEQUENCE	244 AA;	244					
SO		SEQUENCE	244 AA;	26127 MW;	4BI	F17868338F2BF	CRC64;		
Query Match									
Best Local Similarity				49.3%;	Score	641;	DB	2;	Length
Matches				131;	Conservative	36;	Mismatches	72;	Indels
								8;	Gaps
Qy		1	QVQLVESGGGLVQPGGSLRLSCAASGFTFRYSAMSWVQAPRGKGLEWYSAISGRDNTYY	60					
Db		1	QVQLVQSAEAVKPPDSVSKASGAYTFSDDHYMMVQAPOQGLEMMGWIDPNNNDTRF	60					
Qy		61	ADSVKGRFTISRDNSKNTLYIQOMNSLRADFTAVVYCAK--MTSNAPAFDPYWGQGLTVYSS	118					
Db		61	AQRFGRVYTMTRDNTISAAYMEVSRISRSDTAVVYCAABGTSALYGMQWQGLTVYSS	120					
Qy		119	SGGGSGGGGGGGSGQSVLTQPS-VSGAPGQRYTISCTGSSSNIGAGYGVHWYQQLPG	177					
Db		121	SGGGSGGGGGGGSGSDIQMTQSPSTLSASIGDRVITTCRASE---GIYHWLAWYQOKRG	177					
Qy		178	TAPKLLIYGNTRPSPGVDPDFSGFSGTSASLAITGLQAEDEADYICQFYDSSLGCVPG	237					
Db		178	KAPKLLIYKASLAGAPSRFSGSGSDIFLLTISLQPDPAFYTCQY--SNYPPLTG	235					

QY	238	GGTKLTV	244
Db	236	GGTKLEI	242

RESULT 6

ID	Q7TQM2	PRELIMINARY;	PRT;	243 AA.
DT	01-OCT-2003 (TREMBlrel. 25, Created)			
DT	01-OCT-2003 (TREMBlrel. 25, Last sequence update)			
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)			
GN	ScfV_6H8 protein (Fragment).			
OS	Name=scfV_6H8;			
OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	STRAIN=Balb/C.			
RX	MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;			
RA	Peter J.C., Eteharat P., Billiald P., Malikat G., Hoebeke J.;			
RT	"scfV single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor.";			
RL	J. Biol. Chem. 278:36740-36747(2003).			
DR	EMBL; AJ574851; CAE00495.1; -.			
DR	HSEF; F01751; IAGW.			
DR	InterPro; IPR007110; Ig-1like.			
DR	InterPro; IPR003596; Ig_v.			
DR	SMART; SM00406; IGV; 2.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
FT	NON TER			
SQ	SEQUENCE 243 AA; 25976 MW; BEFF64D2DCFAF76 CRC64;			

Query Match 45.6%; Score 593; DB 2; Length 243;  
 Best Local Similarity 51.0%; Pred. No. 6e-34;  
 Matches 125; Conservative 33; Mismatches 77; Indels 10; Gaps 4

QY	1	QVQLVESGGGV	QPGSGSLR	LSGAAGFTR	SRAMSWVRQAP	PKGLGWSAISGR	GNITY	60
Db	1	QVQLQSSSESLVR <td>PAASVRLS<td>CKASGYFT<td>TYWMHWKQRH<td>QGLEMINIT<td>PGSGITNY<td>60</td></td></td></td></td></td>	PAASVRLS <td>CKASGYFT<td>TYWMHWKQRH<td>QGLEMINIT<td>PGSGITNY<td>60</td></td></td></td></td>	CKASGYFT <td>TYWMHWKQRH<td>QGLEMINIT<td>PGSGITNY<td>60</td></td></td></td>	TYWMHWKQRH <td>QGLEMINIT<td>PGSGITNY<td>60</td></td></td>	QGLEMINIT <td>PGSGITNY<td>60</td></td>	PGSGITNY <td>60</td>	60

61 ADSVYGRFTTISRDNSKNTLYIQOMSIARADITYCAKMTSNAFAFDYWGQGLTVVSSG 120  
 61 DEKFNKGLITVDITSSSTAIRYHLLSSLASDSNAVYCAR---GGRGLDVGAGCTTLTVSSG 117  
 121 GGGSGGGSGGGGSGQSGLVLTQ-PPSVSGAPGQRFVITISCTGSSSNIGAGYVHWYQQLPGR 179  
 118 GGGSGGGSGGGGSGSDIQMTQSSSFVSISGRVITITCKASEDIYNR---LAWYQKRGNA 174  
 180 PKLLIYGNTPSPGVPDRPFGSGKSGTSSALATIGQAEPEADYIYQCFYSSLSGWFPGG 239  
 175 PRLISGATISLETGVSPRFGSGSGSKDYTLISLTQEDVATYIYCCQYWMSTR--FGGG 231  
 240 TKLTV 244  
 232 TKLEI 236

RESULT 7

ID	Q921A6	PRELIMINARY;	PRT;	241 AA.
AC	Q921A6;			
DT	01-DEC-2001 (TREMBlrel. 19, Created)			
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)			
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)			
DE	Anti-CBA 79 single chain Fv (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			

RN [1]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=98170165; PubMed=9509426;  
 RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,  
 RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;  
 RT "Cloning and characterization of cDNAs encoding VH and VL of a  
 RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and  
 RT generation of a single-chain Fv molecule (scFv).";  
 RL Mol. Cells 7:816-819(1997).  
 DR EMBL, U88067; AAB48044.1; -.  
 DR PIR, S19965; S19965.  
 DR PIR, S19967; S19967.  
 DR PIR, S19968; S19968.  
 DR PIR, S26325; S26325.  
 DR HSSP, P01607; 1BMW.  
 DR SMART, SMO0406; IGV, 2.  
 DR PROSITE, PSS0835; IG\_LIKE, 2.  
 FT NON\_TER  
 FT NON\_TER 1  
 SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 45.5%; Score 592; DB 2; Length 241;  
 Best Local Similarity 50.8%; Pred. No. 7e-34;  
 Matches 128; Conservative 31; Mismatches 67; Indels 26; Gaps 8;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTPRSYAMSWVRQAPGKLEWVSATISGRDNTY- 59  
 DB 1 QVQLQOSGDELKPKPSTVSKSCASGYFTDYGMNWKQAPGKLEWGMV-----NTYT 55  
 QY 60 ----YADSVKGRFTISRDNSKNTLYIQMNSLRPEDTAVYCAKMTSNAPFDYWGQTLV 115  
 DB 56 GEPYADDFKGRPAFLETSASPAVYQINNLKNEEDATYFCARKDLIR-FTYWGQTLV 114  
 QY 116 TVSSGGGSGGSGGSGGSGGSGQSVLTQ-PPSVGAPGQRTVITSGSSSNIGAGYVHWYQ 174  
 DB 115 TVSSGGGSGGSGGSGGSGGSDIELTQSPSLSSLSGKVTITTCASGD---INKYIANYQH 171  
 QY 175 LFGTAPK---LIYGNTPRSGVDPDRFSGFKSGTISASLAITGLQAEDEADYVQCFYDSS 230  
 DB 172 KKGKGRSRAHTLHY-----IQGIPSRFSGSGSGRDYSPSISNLEPEDYATYCYLHYDNL 227  
 QY 231 LSGWVFGGTXL 242  
 DB 228 ---HTFGGGTXL 236

## RESULT 8

0652L2 PRELIMINARY; PRT; 487 AA.

AC 0652L2;  
 DT 25-OCT-2004 (Tremblrel. 28, Created)  
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
 DE FV/M4.  
 GN Name=M4-IFN- $\epsilon$ tau>;  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96272580; PubMed=8668499;  
 RA Qi Y., Xiang J.;  
 RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric  
 RT antibody secreted from myeloma cells";  
 RL Hum. Antibodies Hybridomas 6:161-166(1995).  
 DR EMBL, S82493; AAB37424.2; -.  
 DR InterPro, IPR003599; IG.  
 DR InterPro, IPR007110; IG\_1like.  
 DR InterPro, IPR003597; IG\_c1.  
 DR InterPro, IPR003598; IG\_c2.  
 DR InterPro, IPR003006; IG\_MHC.  
 DR InterPro, IPR003596; IG\_v.

DR Pfam, PF07654; Cl\_sec. 2.  
 DR Pfam, PF00047; Ig; 4.  
 DR SMART, SMO0409; IG; 3.  
 DR SMART, SMO0407; IGC1; 2.  
 DR SMART, SMO0408; IGC2; 2.  
 DR SMART, SMO0406; IGV, 2.  
 DR PROSITE, PSS0835; IG\_LIKE, 4.  
 DR PROSITE, PSS0290; IG\_MHC; UNKNOWN 1.  
 SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F3055504 CRC64;

Query Match 45.2%; Score 587; DB 2; Length 487;  
 Best Local Similarity 48.0%; Pred. No. 3.3e-33;  
 Matches 119; Conservative 42; Mismatches 69; Indels 18; Gaps 6;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTPRSYAMSWVRQAPGKLEWVSATISGRDNTY 60  
 DB 20 QVQLQSDAEIVKPGASVYKISCKASGYFTDHAHMAKQKPGLEWIGVISPNDIKY 79  
 QY 61 ADSVYKGRFTISRDNSKNTLYIQMNSLRPEDTAVYCAKMTSNAPFDYWGQTLVSSG 120  
 DB 80 NEKFKKATLTITADKSSSTAYMQINLTSDESAVYFCKRS-----YGHWGQGTTLT-GSG 133  
 QY 121 GGGSGGSGGSGGSGGSGQSVLTQ-PPSVGAPGQRTVITSGSS--SNIGAGYVHWYQOLP 176  
 DB 134 GGGSGGSGGSGGSGGSGRIQMTQSPASLSVSGELVITTCRASENTYINLA-----WYQKQ 187  
 QY 177 GAPLLLIYGNTPRSGVDPDRFSGFKSGTISASLAITGLQAEDEADYVQCFYDSSLSGWYF 236  
 DB 188 GKSQQLVYAAINLADGVPSRFRSGSGSGTQVSLKINSIQSEDFGSGYQHFNG--TPYTF 245  
 QY 237 GGGTXLTV 244  
 DB 246 GGGTRLRI 253

## RESULT 9

06GMX4 PRELIMINARY; PRT; 236 AA.

AC 06GMX4;  
 DT 05-JUL-2004 (Tremblrel. 27, Created)  
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE= spleen;  
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,  
 RA Stabileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Bouffard G.G.,  
 RA Raha S.S., Lochuallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Kravitz M.I., Skalska U., Smalios D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.



RC TISSUE=Splicein;  
 RA Strauberg R.;  
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, BC073769; AAH73769.1; -  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PR07654; Cl-set; 1.  
 DR Pfam; PR00047; IG; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR Hypothetical protein.  
 KW SEQUENCE 236 AA; 24809 MW; BA0AF0F4192364A5 CRC64;

Query Match 42.5%; Score 553; DB 2; Length 236;  
 Best Local Similarity 91.4%; Pred. No. 3.7e-31;  
 Matches 106; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 131 GGGSGSVLTQPSVSGAPGQRTVTSCTGSSSNIGAGYGVHWYQQLPGTAPKLLIYGNTR 190  
 DB 16 GSWAGSVLTQPSVSGAPGQRTVTSCTGSSSNIGAGYGVHWYQQLPGTAPKLLIYGNTR 75  
 QY 191 PGVPDRFSGKSGTSASLAITGLQAEDEADYCCQYDSSLSGWSVGGGKTLTVLG 246  
 DB 76 PGVPDRFSGKSGTSASLAITGLQAEDEADYCCQYDSSLSGWSVGGGKTLTVLG 131

## RESULT 10

Q96BB9 PRELIMINARY; PRT; 597 AA.

AC Q96BB9; PRELIMINARY; PRT; 597 AA.  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE IGHM protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stachenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson J.D., Mullany S.J.,  
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schmech A., Schein U.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strauberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL, BC015760; AAH15760.1; -  
 DR PIR; S05271; S05271.  
 DR PIR; S24260; S24260.  
 DR HSSP; P01861; IADQ.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PR07654; Cl-set; 4.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 DR SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

Query Match 41.2%; Score 535; DB 2; Length 597;  
 Best Local Similarity 52.6%; Pred. No. 1.8e-29;  
 Matches 122; Conservative 19; Mismatches 55; Indels 36; Gaps 5;

QY 1 QVOLVESGGGLVQPGSLRLSCAAGFTFRSYAMSVWRQAPGKLEWVAISGRGNTYY 60  
 DB 20 EQVLESGLVQPGSLRLSCAAGFTFRSYAMSVWRQAPGKLEWVAISGGGNTYY 79  
 QY 61 ADSVKGRFTISDNRKNTLYLQNSLRADTVAYYCAK-----MTSNAFADYQCGTL 114  
 DB 80 ADSVKGRFTISDNRKNTLYLQNSLRADTVAYYCAKDPGYSAGNTREDYWGQCTL 139  
 QY 115 VTVSSGGGGGGGGGGGGSSQSVLTQPSVSGAPGQRTVTSCTGSSSNIGAGYGVHWYQ 173  
 DB 140 VTVSSGS-----ASAPTLFPLVSCENSPSDTSVAVAGCLAOD 176  
 QY 174 QLPGTAPKLLIYGNTRPS---GVDPDRFSGKSGTSASLAITG---LQADE 219  
 DB 177 FLDPSTFSGKTKKNSDISSTRGFPVSLGKRYATSGYVTLPSKDVQGTDE 228

## RESULT 11

Q925S1 PRELIMINARY; PRT; 218 AA.

AC Q925S1; PRELIMINARY; PRT; 218 AA.  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE MRPS (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX PubMed=11819679;  
 RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
 RA Su C.;  
 RT "Mechanism of exogenous nucleic acids and their precursors improving  
 the repair of intestinal epithelium after irradiation in mice.";  
 RL World J. Gastroenterol. 6:709-717(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RT Cui D., Zeng G., Yan X., Li X., Su C.;  
 RT "Cloning of mouse genes related to repairing of intestinal epithelium  
 of the irradiated mice by treatment with the intestinal RNA of mice of  
 the same strain.";  
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
 DR EMBL; AF240168; AAK43733.1; -  
 DR HSSP; P01665; IONZ.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR NON TER 218  
 SQ SEQUENCE 218 AA; 23013 MW; 527B4FA8F7982817 CRC64;

Query Match 40.6%; Score 527.5; DB 2; Length 218;  
 Best Local Similarity 51.4%; Pred. No. 2.1e-29;

Matches 110; Conservative 32; Mismatches 67; Indels 5; Gaps 4;

QY 1 OYVLSGGGGLVOPQSGSLRLSCASGFTSRYSAMSVNRQAPKGLKEMWASIGRQNTY 60  
 Db 3 QYVLOQSGGELKPKPGFTVRISCAASGYTTTGMOMVQKPGKLMIMVHSGVPRY 62  
 QY 61 ADSVKKRFTISRDNKNTLYLQNNSLRADTAVYVCARKNTSNAFADYWGQGLTVTVSSG 120  
 Db 63 AAEFKRFAFSLSTASTAYLQSNKNEDTATYFCMRWDYDG-GRAYWGQGTITVTVSSG 121  
 QY 121 GGGSGGGSGGGGGSGSGLTQ-PPSVSGAPGQRTVISTCTSSG--NTGAGYGVHWYQQLPG 177  
 Db 122 GGGSGGGSGGGSGSGLTQSPASLAVSLGQRTATISCRASESYDNIGISF-MWVFOQKPG 180  
 QY 178 TAPKLLIYNTNPPSGVDPDRFSGSGKSGTSASLAI 211  
 Db 181 QPKLLIYASKQSGGVAGLASSGSDTPSLNT 214

RESULT 12

Q6GMX3 PRELIMINARY; PRT; 236 AA.

AC Q6GMX3; 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loeuallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073770; AAH73770.1; -  
 DR InterPro; IPR003599; IG\_1  
 DR InterPro; IPR007110; IG\_1like  
 DR InterPro; IPR003597; IG\_1  
 DR InterPro; IPR003006; IG\_MHC  
 DR InterPro; IPR003596; IG\_V  
 DR Pfam; PF00654; Cl-set; 1.  
 DR Pfam; PF00647; IG\_2  
 DR SMART; SM00409; IG\_2  
 DR SMART; SM00407; IG1; 1.  
 DR SMART; SM00406; IG1; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.

KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 24700 MW; BC0B394DF4F2DCB7 CRC64;

Query Match 40.2%; Score 523; DB 2; Length 236;  
 Best Local Similarity 87.8%; Pred. No. 4.7e-29;  
 Matches 101; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 131 GGGSGSVLTQPPSVSGAPGQRTVISTCTSSSSNIGAGYGVHWYQQLPGTAPKLLIYNTNR 190  
 Db 16 GSMASVLTQPPSVSGAPGQRTVISTCTSSSSNIGAGYGVHWYQQLPGTAPKLLIYNTNR 75  
 QY 191 PEGVDPDRFSGSGKSGTSASLAIAGLQAEDEADYTCQYDSSLSGWFPGGTITVL 245  
 Db 76 PEGVDPDRFSGSGKSGTSASLAIAGLQAEDEADYTCQYDSSLSGWFPGGTITVL 130

RESULT 13

Q96E61 PRELIMINARY; PRT; 236 AA.

AC Q96E61; 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loeuallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC012876; AAH12876.1; -  
 DR PIR; S12440; S12440.  
 DR HSSP; P01842; IAOK.  
 DR InterPro; IPR007110; IG\_1like  
 DR InterPro; IPR003597; IG\_1  
 DR InterPro; IPR003006; IG\_MHC  
 DR InterPro; IPR003596; IG\_V  
 DR Pfam; PF00654; Cl-set; 1.  
 DR Pfam; PF00646; IG1; 1.  
 DR SMART; SM00406; IG1; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match 39.8%; Score 518; DB 2; Length 236;  
 Best Local Similarity 85.3%; Pred. No. 1.1e-28;

Matches 99; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 131 GGGSGGVLTPPSVSGAPGQRTVTSCTGSSSNIGAGYGVHWYQOLPRTAPKLIYNTNR 190

DB 16 GSWAGCVLAPPSVSGAPGQRTVTSCTGSSSNIGAGYGVHWYQOLPRTAPKLIYNTNR 75

QY 191 PGVPRPFGSGTSGTASLAITGLQAEDEADYTCQYDSSLGSMVGGGKTLVLG 246

DB 76 PGVPRPFGSGTSGTASLAITGLQAEDEADYTCQYDSSLGSMVGGGKTLVLG 131

## RESULT 14

Q9WUK1 PRELIMINARY; PRT; 613 AA.

AC Q9WUK1; 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

OS Homo sapiens (Human).

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI\_Taxid=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,

RA Stachewicz M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ueda T.B., Tohyuki S., Carninci P., Prange C.,

RA Rabe S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Millar S.J.,

RA Boeck S., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Maier M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."

RU Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RA Strausberg R.L.

Best Local Similarity 52.8%; Pred. No. 3.1e-28;

Matches 120; Conservative 14; Mismatches 62; Indels 31; Gaps 5;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTPRSAVSVAWROAPKGLKLEWVSAISRGRDNTY 60

DB 20 QVQLVESGGGLVQPGGSLRLSCAASGFTPRSAVSVAWROAPKGLKLEWVSAISRGRDNTY 79

QY 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIVYCAKMTSNAF-AFDYWGQGLTVVSS 119

DB 80 ADSVKGRTISRDNKNTLYIQMNSLRADTAIVYCAKMTSNAF-AFDYWGQGLTVVSS 139

QY 120 GGGSGGGGGGGGSGSVLTTPPSVSGAPGQRTVTSCTGSSSNIGAGYGVHWYQOLPRT 178

DB 140 GS-----ASAPTLPLPVSCNSPDTSSVAVGCLAQPLPDS 176

QY 179 APKLIYNTNRP-----GVPRPFGSGTSGTASLAITG---LOAEDE 219

DB 177 TFSWKYKNSDISSTRGFPVLRGKTAATSVQVILPSKDVWGIDE 223

## RESULT 15

Q9UL71 PRELIMINARY; PRT; 121 AA.

AC Q9UL71; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

OS Myosin-reactive immunoglobulin heavy chain variable region

DE (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI\_Taxid=9606;

RP SEQUENCE FROM N.A.

RC MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;

RA Wu X., Liu B., Van der Merwe P.L., Kalls N.N., Berney S.M.,

RA Young D.C.,

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus."

RU Clin. Immunol. Immunopathol. 87:184-192(1998).

RA EMBL; AF035043; AAD56279.1; --

RA HSSP; P01852; INFD.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG\_LIKE; 1.

FT NON\_TER 1 121

FT NON\_TER 1 121

SEQUENCE 121 AA; 13154 MW; 2F045CCFASD50736 CRC64;

Query Match 38.8%; Score 505; DB 2; Length 121;

Best Local Similarity 81.8%; Pred. No. 4.3e-28;

Matches 99; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTPRSAVSVAWROAPKGLKLEWVSAISRGRDNTY 60

DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTPRSAVSVAWROAPKGLKLEWVSAISRGRDNTY 60

QY 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIVYCA--KMTSNAPFDYWGQGLTVVSS 118

DB 61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIVYCAKMTSNAPFDYWGQGLTVVSS 120

QY 119 S 119

DB 121 S 121

Search completed: April 19, 2005, 16:43:13

Job time : 120.967 secs

Query Match 39.8%; Score 517.5; DB 2; Length 613;

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2005, 16:23:17 ; Search time 120.008 Seconds  
(without alignments)  
779.913 Million cell updates/sec

Title: US-09-250-056B-2

Sequence: 1 QVQLVSGGGLVQPGGSLRLT.....QQYNSTPLSFSGGTKEIKR 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1980s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1267	100.0	242	3	AA58236 Internal
2	1084.5	85.6	239	7	ADG30447 Human GMB
3	1069	84.4	231	8	ADN06993
4	1065.5	84.1	233	4	AA65715 Antio
5	1060.5	83.7	247	5	ABP45912 Human Bly
6	1058.5	83.5	239	5	ABP45911 Human Bly
7	1058.5	83.5	239	5	ADG96738 Single ch
8	1057.5	83.5	239	5	ADG96738 Single ch
9	1057.5	83.5	245	8	ADG96738 Single ch
10	1057.5	83.5	245	8	ADG96738 Single ch
11	1051.5	83.0	243	8	ADG96738 Single ch
12	1050.5	82.9	239	5	ABP45871 Human Bly
13	1050.5	82.9	239	5	ADG96698 Single ch
14	1050.5	82.9	248	5	ABP45410 Human Bly
15	1050.5	82.9	248	5	ADG96237 Single ch
16	1048	82.7	240	4	AA646038 Human TF
17	1047	82.6	240	2	AA502472 A single
18	1047	82.6	240	6	ABP95997 Human ser
19	1047	82.6	240	8	ADL92369 Human pha
20	1047	82.6	240	8	ADQ77165 HSA Heavy
21	1046	82.6	242	8	ADQ75289 Immunoglo
22	1046	82.6	250	8	ADQ40407 Single ch
23	1044.5	82.4	244	8	ADQ75290 Immunoglo
24	1044	82.4	240	7	ADG30465 Human GMB
25	1043.5	82.4	243	5	ABP45924 Human Bly

26	1043.5	82.4	243	7	ADG96751 Single ch
27	1041	82.2	240	4	AA646007 Human MUC
28	1041	82.2	249	8	ADQ40411 Single ch
29	1041	82.2	250	8	ADQ40410 Single ch
30	1040.5	82.1	245	2	AA506714 Antibody
31	1040.5	82.1	245	8	ADQ39733 Human c-m
32	1040.5	82.1	251	5	ABP45299 Human Bly
33	1040.5	82.1	251	7	ADG96126 Single ch
34	1040	82.1	241	2	AAW24063 Human WSX
35	1040	82.1	241	7	ADQ08951 Human MSX
36	1039	82.0	291	8	ADN06992 Human ERG
37	1037	81.8	240	4	AA646039 Human TF
38	1034	81.6	240	4	AA646040 Human TF
39	1033.5	81.6	243	5	ABP45934 Human Bly
40	1033.5	81.6	243	7	ADG96761 Single ch
41	1032	81.5	239	5	AAU90905 Immunin/1
42	1032	81.5	240	4	AA646020 Human MUC
43	1031	81.4	244	5	ABP44071 Human Bly
44	1031	81.4	244	7	ADG94898 Single ch
45	1030	81.3	240	4	AA645999 Human MUC

## ALIGNMENTS

RESULT 1	AA58236	standard; protein; 242 AA.
ID	AA58236	
AC	AA58236;	
DT	27-MAR-2000	(first entry)
XX		
DE	Internalising anti-c-erbB-2 receptor antibody scFv C1.	
XX		
KW	Antibody; c-erbB-2 receptor; marker; cancer; drug targeting;	
KW	HER/neu oncogene; tumour-specific; internalisation; non-immunogenic.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	Region	31..35
FT	Region	/note="Heavy chain variable region (VH) complementarity determining region 1 (CDR1)"
FT	Misc-difference	37
FT	Region	/note="Encoded by GIM"
FT	Region	50..66
FT	Region	/note="VH-CDR2"
FT	Region	99..108
FT	Region	/note="VH-CDR3"
FT	Region	158..168
FT	Region	/note="Light chain variable region (VL) complementarity determining region 1 (CDR1)"
FT	Region	184..190
FT	Region	/note="VL-CDR2"
FT	Region	223..231
FT	Region	/note="VL-CDR3"
XX		
XX	WO995367-A1.	
XX	04-NOV-1999.	
XX	23-APR-1999;	99WO-US007395.
XX	24-APR-1998;	98US-0082933P.
XX	PR 12-FEB-1999;	99US-00250056.
XX	(REGC ) UNIV CALIFORNIA.	
XX	Marka JD, Poul MA;	
XX	WPI; 2000-072168/06.	

DR N-PSDB; AA255615.

XX Novel internalizing antibodies used to treat cancer cells.

XX Claim 3; Page 82; 85pp; English.

XX This sequence represents an internalizing humanised antibody, scFv C1, which specifically binds to the extracellular domain of the c-erbB-2 receptor, the protein product of the HER/neu oncogene. The scFv C1 antibody binds to the epitope of the c-erbB-2 receptor that is bound by C1 antibodies. On binding the c-erbB-2 receptor, the antibody is transported into the cell. The c-erbB-2 receptor is a marker protein which is overexpressed by 30-50% of breast carcinomas and other adenocarcinomas, and thus provides a useful cell surface marker for specifically targeting tumour cells. The antibodies of the invention are used as tumour-targeting molecules for diagnosis and treatment. The antibodies can be attached to effector molecules. The effector molecules may include cytotoxins such as ricin, abrin or Pseudomonas exotoxin, radionuclides, ligands such as growth factors, therapeutic agents such as vinblastine, vindesine or melphalan; ribozymes; or antisense molecules. The antibodies may also be used for in vivo or in vitro detection and/or quantitation of the c-erb-2 receptor and thus diagnosis and/or localisation of cancers characterised by expression of c-erb-2. Although antibodies have previously been used to target tumour cells, their success has been limited. The utility of prior art antibodies has been hampered by the paucity of tumour specific antibodies, antibody immunogenicity, low binding affinity, and poor tumour penetration. Immunogenicity could be avoided and toxicity reduced if high affinity tumour specific human antibodies were available. However, the production of human monoclonal antibodies using conventional hybridoma technology has proven difficult. Also, most of the antibodies produced react with antigens that are also common to non-malignant cells, which makes them unsuitable for use as tumour-targeting molecules. The antibodies of the invention overcome these difficulties, as they are targeted to a tumour-specific antigen, and avoid the problem of immunogenicity as they are human in origin.

XX Sequence 242 AA;

Query Match 100.0%; Score 1267; DB 3; Length 242;  
Best Local Similarity 100.0%; Pred. No. 5.7e-82;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVSGGGLVQPGSLRLSCAASGFTSSYAMGVWROAPKGLEWVSISGSSRYIY 60  
DB 1 EVQLVESGGGLVQPGSLRLSCAASGFTSSYAMGVWROAPKGLEWVSISGSSRYIY 60  
QY 61 ADSVGRFTISRDNKNTLYLQNSLRADTAIVYCAKMDAGSYNPNFGQGLTVTVSSG 120  
DB 61 ADSVGRFTISRDNKNTLYLQNSLRADTAIVYCAKMDAGSYNPNFGQGLTVTVSSG 120  
QY 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 180  
DB 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 180  
QY 181 LIYAASLTQGVPSRFSGSGGTDTLTLSIQPEDPATYVCOQNSYPLSFGGKTKVEI 240  
DB 181 LIYAASLTQGVPSRFSGSGGTDTLTLSIQPEDPATYVCOQNSYPLSFGGKTKVEI 240  
QY 241 KR 242  
DB 241 KR 242

RESULT 2

ID ADG30447 standard; protein; 239 AA.

XX ADG30447;

XX 26-FEB-2004 (first entry)

DE Human GMB655 scFv protein.

XX GMAD; VH; CDR; complementarity determining region; VL; scFv;  
KW single chain antibody; antidiabetic; type II diabetes; human; GMB655.  
XX Homo sapiens.XX WO2003085093-A2.  
XX 16-OCT-2003.  
XX 28-MAR-2003; 2003WO-US009625.  
XX 01-APR-2002; 2002US-036813P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Baker KP, Albert VR, Chowdhury P;  
XX WPI, 2003-804305/75.  
XX N-PSDB; ADG30544.  
XX New antibody that specifically binds to GMAD polypeptide, useful for  
PT diagnosing, monitoring, treating, preventing or ameliorating type II  
PT diabetes.  
XX Claim 2; SEQ ID NO 80; 410pp; English.

XX The invention relates to a novel antibody that specifically binds to a  
CC GMAD polypeptide comprising a first amino acid sequence that is at least  
CC 95% identical to a second amino acid sequence of a VH CDR (single chain  
CC (complementarity determining region) or VL CDR of an scFv (single chain  
CC antibody molecule). The antibody of the invention demonstrates  
CC antidiabetic activity and may be useful for diagnosing, monitoring,  
CC treating, preventing or ameliorating type II diabetes. The current  
CC sequence is that of the human scFv protein of the invention.

XX Sequence 239 AA;

Query Match 85.6%; Score 1084.5; DB 7; Length 239;  
Best Local Similarity 85.1%; Pred. No. 4.7e-69;  
Matches 206; Conservative 16; Mismatches 17; Indels 3; Gaps 1;

QY 1 QVQLVSGGGLVQPGSLRLSCAASGFTSSYAMGVWROAPKGLEWVSISGSSRYIY 60  
DB 1 EVQLVESGGGLVQPGSLRLSCAASGFTSSYAMGVWROAPKGLEWVSISGSSRYIY 60  
QY 61 ADSVGRFTISRDNKNTLYLQNSLRADTAIVYCAKMDAGSYNPNFGQGLTVTVSSG 120  
DB 61 ADSVGRFTISRDNKNTLYLQNSLRADTAIVYCAKMDAGSYNPNFGQGLTVTVSSG 117  
QY 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 180  
DB 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 177  
QY 181 LIYAASLTQGVPSRFSGSGGTDTLTLSIQPEDPATYVCOQNSYPLSFGGKTKVEI 240  
DB 181 LIYAASLTQGVPSRFSGSGGTDTLTLSIQPEDPATYVCOQNSYPLSFGGKTKVEI 237  
QY 241 KR 242  
DB 238 KR 239

RESULT 3

ID ADN06993 standard; protein; 291 AA.

XX ADN06993;

XX 01-JUL-2004 (first entry)

DE Human ERGR bs-scFv antibody protein, EGFR.B8.



CC transport ligands such as antibodies and/or to deliver biologically  
CC active components such as proteins, nucleic acids or detectable labels.  
CC They are used to deliver therapeutic compositions to mucosal surfaces  
CC such as the gastro-intestinal tract, respiratory system etc. in humans.  
CC They are also useful to label cells expressing pIgR, e.g. to distinguish  
CC epithelial cells from a mixed cell population in pathology studies or to  
CC aid in carcinoma diagnosis (since pIgR expression is reduced in  
CC carcinomas relative to normal epithelium). They can also be used to  
CC deliver veterinary compositions, especially in mammals such as farm,  
CC domestic or wild mammals or birds e.g. birds reared for human  
CC consumption. The present sequence represents the amino acid sequence of  
CC secreted form of scFv 4A  
XX  
SQ Sequence 293 AA;

Query Match 84.1%; Score 1065.5; DB 4; Length 293;  
Best Local Similarity 84.8%; Pred. No. 1.3e-67;  
Matches 206; Conservative 12; Mismatches 24; Indels 1; Gaps 1;

QY 1 QVQLVESGGGLVQPQGSRLRLSCAAGFTFSYAMGVWROAPGKLEWVSSISGSRYY 60  
DB 28 QVQLVQSGGGLVQPQGSRLRLSCAAGFTFSYAMGVWROAPGKLEWVSAISGSGSTYY 87  
QY 61 AASVKGRTFTSRDNRNTLYLQNSLRADTAIVYCAK--MDASGSYFNWGQTLVTVSS 119  
DB 88 ADSVKGRTFTSRDNRNTLYLQNSLRADTAIVYCAKSFYVNSGYFGHMGQTLVTVSS 147  
QY 120 GGGSGGGSGGGSGGSETTLTQSPFLSAFVDRITTCRASPCIRNYLAWYQOKPKAKP 179  
DB 148 GGGSGGGSGGGSGGSETTLTQSPFLSAFVDRITTCRASPCIRNYLAWYQOKPKAKP 207  
QY 180 LIIVAASTLQSGVPSRFSGSGGTDTFTLTISLQPEDPATYVCCQYNSYPLSFGGTXYE 239  
DB 208 LIIVKASISLQSGVPSRFSGSGGTDTFTLTISLQPEDPATYVCCQYNSYPLSFGGTXYD 267  
QY 240 IKR 242  
DB 268 IKR 270

RESULT 5  
ABP45912  
ID ABP45912 standard; protein; 247 AA.

AC ABP45912;  
XX  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human BlyS binding scFv SEQ ID 1923.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytosolic;  
XX tumour necrosis factor; B cell proliferation; B cell differentiation;  
XX immunosuppressive; immunomodulatory; antirheumatic;  
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX MO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
PI WPI; 2002-114799/15.  
XX

PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 2695-2696; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
CC and so may be used to detect and quantitate the presence of BlyS in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of BlyS. They may also be  
CC administered to treat diseases associated with aberrant BlyS expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention

SQ Sequence 247 AA;

Query Match 83.7%; Score 1060.5; DB 5; Length 247;  
Best Local Similarity 82.2%; Pred. No. 2.4e-67;  
Matches 203; Conservative 20; Mismatches 19; Indels 5; Gaps 2;

QY 1 QVQLVESGGGLVQPQGSRLRLSCAAGFTFSYAMGVWROAPGKLEWVSSISGSRYY 60  
DB 1 EVQLVQSGGGLVQPQGSRLRLSCAAGFTFSYAMGVWROAPGKLEWVSAISGSGSTYY 60  
QY 61 ADSVKGRTFTSRDNRNTLYLQNSLRADTAIVYCAKMDA--SGS--YFNWGQTLV 115  
DB 61 ADSVKGRTFTSRDNRNTLYLQNSLRADTAIVYCAKMDA--SGS--YFNWGQTLV 120  
QY 116 TVSSGGGGSGGGSGGSETTLTQSPFLSAFVDRITTCRASPCIRNYLAWYQOKXG 175  
DB 121 TVSSGGGGSGGGSGGSETTLTQSPFLSAFVDRITTCRASPCIRNYLAWYQOKXG 180  
QY 176 KAPKLLIYAASTLQSGVPSRFSGSGGTDTFTLTISLQPEDPATYVCCQYNSYPLSF 235  
DB 181 KAPKLLIYAASTLQSGVPSRFSGSGGTDTFTLTISLQPEDPATYVCCQYNSYPLSF 240  
QY 236 TVVEIKR 242  
DB 241 TKLKIKR 247

RESULT 6  
ADG96739  
ID ADG96739 standard; protein; 247 AA.

XX ADG96739;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds BlyS SeqID 1923.

XX antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;

XX B cell proliferation; differentiation; scFv; myasthenia gravis;

XX multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;

XX carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;

XX antinflammatory; antiaesthetic; antiallergic; cytostatic.

XX Unidentified.



PN WO2003055979-A2.  
 XX  
 XX 10-JUL-2003.  
 XX  
 PF 14-NOV-2002; 2002WO-US036496.  
 XX  
 PR 16-NOV-2001; 2001US-0331469P.  
 PR 19-DEC-2001; 2001US-0340817P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;  
 XX  
 DR WPI; 2003-505530/47.  
 XX  
 PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
 PT (Blys), useful for detecting and treating diseases or disorders e.g.  
 PT rheumatoid arthritis, asthma and leukemia.  
 XX  
 PS Example 1; SEQ ID NO 1923; 394pp; English.

CC This invention relates to novel antibodies that immunospecifically bind  
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to  
 CC chromosome 13q34 and encodes a protein that is a member of the tumour  
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
 CC proliferation and differentiation. Specifically, it refers to single  
 CC chain antibody molecules (scFvs) derived, preferably, from the variable  
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
 CC fragment thereof, of either human, murine, rat or monkey Blys. The  
 CC present invention refers to the use of such antibodies in various methods  
 CC for the detection, diagnosis and prognosis of diseases related to the  
 CC aberrant expression or inappropriate function of Blys or its receptor. As  
 CC such, these compositions are useful for identifying immune disorders  
 CC including myasthenia gravis and multiple sclerosis, inflammatory  
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
 CC lymphoma. Accordingly, they can be described as exhibiting various  
 CC activities such as antirheumatic, antiarthritic, neuroprotective,  
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This  
 CC polypeptide sequence is a single chain antibody that binds Blys of the  
 CC invention. NOTE: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published pct\_sequences.

CC Sequence 247 AA;

Query Match 83.7%; Score 1060.5; DB 7; Length 247;  
 Best Local Similarity 82.2%; Pred. No. 2,4e-67;  
 Matches 203; Conservative 20; Mismatches 19; Indels 5; Gaps 2;

QY 1 QVQLVSGGGLVPGGSLRLSCAASGFTFSYAMGWROAPGKGLVWSISGSSRIYY 60  
 DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTFSYAMSWROAPGKGLVWSAISGSGSTYY 60  
 QY 61 ADSVKRFTISRDNKNTLYLQNSLRADDTAVYYCAKMDA---SGS--YFNFGQGLTV 115  
 DB 61 ADSVKRFTISRDNKNTLYLQNSLRADDTAVYYCAKAGNRSGLVYFDWGRRTW 120  
 QY 116 TVSSGGGGSGGGSGGGSEFTTLTQSPSFLSAFVGDRITITTCASPGIRNYLAWYQKPG 175  
 DB 121 TVSSGGGGSGGGSGGGSDIOMTQSPSTLSASIGRVITTCASSEGIRYRLAWYQKPG 180  
 QY 176 KAPKLLIYASTQSGVPSRFSGSGGDTFTLTSSIQEPDFTVYCCQVNSYPLSRGGG 235  
 DB 181 KAPKLLIYKASSLSAGPSRFSGSGGDTFTLTSSIQEPDFTVYCCQVNSYPLSRGGG 240  
 QY 236 TKVEIKR 242  
 DB 241 TKVKIKR 247

RESULT 7  
 ABP45911

ID ABP45911 standard; protein; 239 AA.

XX AC ABP45911;

XX XX 19-AUG-2002 (first entry)

DE Human Blys binding scFv SEQ ID 1922.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX DR WPI; 2002-114799/15.

XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the

XX diagnosis and treatment of cancers and immune disorders.

XX PS Claim 1; Page 2694-2695; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention

XX SQ Sequence 239 AA;

Query Match 83.5%; Score 1058.5; DB 5; Length 239;  
 Best Local Similarity 83.5%; Pred. No. 3.3e-67;  
 Matches 202; Conservative 18; Mismatches 19; Indels 3; Gaps 1;

QY 1 QVQLVSGGGLVPGGSLRLSCAASGFTFSYAMGWROAPGKGLVWSISGSSRIYY 60  
 DB 1 EVQLVETGGGLVPGGSLRLSCAASGFTFSYAMSWROAPGKGLVWSAISGSGSTYY 60  
 QY 61 ADSVKRFTISRDNKNTLYLQNSLRADDTAVYYCAKMDASGSYFNFGQGLTVYSSG 120  
 DB 61 ADSVKRFTISRDNKNTLYLQNSLRADDTAVYYCAK---GWRGVYDWGRGLTVYSSG 117



(TPO). They can stimulate proliferation, differentiation or growth of megakaryocytes. They may also be able to stimulate megakaryocytes to increase platelet production. They can be used for treating immunological or hematopoietic disorders, especially thrombocytopenia. Thrombocytopenia-associated bone marrow hypoplasia (e.g. aplastic anemia following chemotherapy or bone marrow transplant) may be effectively treated with the antibody compounds as well as disorders such as disseminated intravascular coagulation (DIC), immune thrombocytopenia (HIV-induced and non HIV-induced), chronic idiopathic thrombocytopenia, congenital thrombocytopenia, thrombotic thrombocytopenia and myelodysplasia. They can also be used in e.g. myelotoxic chemotherapy for treatment of solid tumours or leukaemia, myeloblastic chemotherapy for autologous or allogeneic bone marrow transplant, myelodysplasia, idiopathic aplastic anemia, congenital thrombocytopenia, and immune thrombocytopenia. The antibodies which bind to the Mxk receptor can be used for improving neuromuscular function in a patient, e.g. in muscular dystrophy. The products can also be used for detection and diagnosis. The antibodies have a longer half-life than the natural ligand for the TPO-R. Sequences AY06713-1-06718 represent single chain Fv (scFv) fragments of various antibodies

**Sequence 245 AA;**

Query Match	83.5%	Score 1057.5;	DB 2;	Length 245;
Best Local Similarity	83.1%	Pred. No. 3.9e-67;		
Matches 201; Conservative	20;	Mismatches 20;	Indels 1;	Gaps 1;

Qy	1	QVQLVESGGGLVQPGGSLRLISCAASGFTFSVYAMGVRRAPGKGLMEVSSI	SSGSSSYIY	60
Db	3	QVQLVESGGGLVQPGGSLRLISCAASGFTFSVSHNMNVRRAPGKGLMEVSSI	SSSSSYIY	62
Qy	61	ADSVYGRFTISRDNSKNTLYLQMNSLRADFTAVYVCAKDDASGSEYENPFGQGLTVVSSG		120
Db	63	ADSVYGRFTISRDNAKNSLYLQMNSLRADFTAVYVCAKDDASGSEYENPFGQGLTVVSSG		121
Qy	121	GGSGGGGSSGGGSETTLTQSPSPFLSAFVGDRTITTCRASTPGIRNLTAVYQKRGKAPKL		180
Db	122	GGSGGGGSSGGGSSDITQMTQSPSTLSASFGDRITTCRASTPGIRNLTAVYQKRGKAPKL		181

Oy 181 LTVASTLQSGVPSPFSGSGSDTFLTISLQPEPATYCCQVQNNYPLSGGGTKYEI 240  
 182 LTVASTLQSGVPSPFSGSGSDTFLTISLQPEPATYCCQVQNNYPLSGGGTKYEI 241  
 Db 182 LTVASTLQSGVPSPFSGSGSDTFLTISLQPEPATYCCQVQNNYPLSGGGTKYEI 241

Qy 241 KR 242  
242 ||  
Db 242 KR 243

RESULT 10  
ADO39736  
ID ADO39736 standard; protein; 245 AA.

AC	ADO39736;	.
XX		
DT	29-JUL-2004	(first entry)

DS	Human c-mpl single chain agonist antibody fragment (scFv) protein, 12D5
XX	
KM	Variable heavy chain; VH; variable light chain; VL; c-mpl antibody; CDR
KM	hemostatic; haemacopoietic disorder; thrombocytopaenia; gene therapy;
KM	antibody; agonist; human; single chain antibody fragment; scFv.

**Homo sapiens.**

FH	Key	Location/Qualifiers
1		

FT	Region	33. .37
FT		

/NOTE= "VH CDR1"

Region	52. .73
FT	
PT	

PT	/note= "VH CDR2"
101	100

```

ET      Region      101. .109
ET      /note= "VH CDB3"

```

ET	Reaction	ET	Reaction
159	/note= "VH CDR3"	159	169

FT	159. .169
FT	/note= "VT, CDR1 "
Region	

FI / note= "VL CDR1"

FT	Region	185..191
FT		/note= "VL CDR2"
FT	Misc-difference	208
FT		/label= Unknown
FT		/note= "Xaa may be any amino acid"
FT	Region	224..232
FT		/note= "VL CDR3"

PN US6737249-B1.

PD 18-MAY-2004.

PF 21-AUG-1998; 98US-00138091.

PR 22-AUG-1997; 97US-0056736P.

PA (GETH ) GENENTECH INC.

PI Adams CW, Carter PJ, Fendly BM, Gurney AL, ...

DR WPI; 2004-387096/36.

PT New nucleic acid encoding human c-mpl agonist antibody comprising Ab1, Ab2, Ab3, Ab4, Ab5 or Ab6, useful in preparing a composition for treating hematopoietic disorders, e.g., thrombocytopenia.

PS Disclosure; SEQ ID NO 76; 58pp; English

CC The present invention relates to human c-mpl antibodies comprising Ab1  
CC Ab2, Ab3, Ab4, Ab5 and Ab6 each of which comprises a VH and VL chain  
CC comprising CDR amino acid sequences designated CDR1, CDR2 and CDR3 and  
CC their encoding nucleic acids. The invention acts as a haemostatic agent  
CC and is useful for treating haematopoietic disorders such as  
CC thrombocytopaenia. The invention is also useful in gene therapy. The  
CC present sequence is human c-mpl single chain agonist antibody fragment  
CC (scFv) protein.

**SQ** Sequence 245 AA;

Query Match	83.5%	Score 1057.5	DB 8	Length 245
Best Local Similarity	83.1%	Pred. No. 3.9e-67		
Matches 201	Conservative 20	Mismatches 20	Indels 1	Gaps 1

Dy 1 QVQVLVESGGGLVPDGGSLRLSCAASGFTSSYAMGWVRQAIPKGLEWVSLSGSSRIYY 60  
|||::|||:  
Db 3 QVQLVESGGGLVKRRGSLRLSCAASGFRTSSHNNHWVRQAIPKGLEWVSSLSSSSSIYY 62

```
Qy      61 ABSVKGRFTISRDNKNTIYLQNNSLRAEDTAIVYCAKDASGSYFNFGGDTLVYSSG 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      63 ABSVKGRFTISRDAKNSLYLQNNSLRAEDTAIVYCAR-DRSGTGMDVWGSGTLVYSSG 121
```

```
Qy      121 GGGSSGGSSGGSSGSETTLTQSPFSLAFVVDRIITTCRASPGIRNVLAWYQQKPGKAPKL 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      122 GGGSSGGSSGGSSGSDIQMTQSPSTLSASIGDRVITTCRASGEGYHMLAWYQQKPGKAPKL 181
```

Qy 181 LIYAASITQSGVSPRFSGSGSGDTFTLTISLQPDFAATYCCQQVNSYPLSFGGGTKEI 240

Db 182 LIYASLASGAPSRFSGSGSGDTFTXTISLQPDFAATYCCQQVNSYPLTFGGGTKEI 241

Qy	241 KR 242
Db	242 KR 243

RESULT 11

ADIS58047

ID ADI58047 standard; protein; 243 AA.

XX  
XX  
ADTCCGAT.

AC ADI58047;  
XX

XX  
DT 22-APR-2004 (Eject output)

DT 22-APR-2004 (first entry)  
XX

Reg IV-specific single chain antibody fragment (scFv) #6:

XX antibody; regeneration IV; Reg IV; single chain antibody fragment; scFv;  
 KW inflammatory bowel disorder; ulcerative colitis; Crohn's disease;  
 KW diabetes; non-insulin dependent diabetes; insulin dependent diabetes;  
 KW cancer; human.  
 OS Homo sapiens.  
 XX  
 XX WO2004003144-A2.  
 XX  
 XX 08-JAN-2004.  
 XX  
 XX 26-JUN-2003; 2003WO-US019908.  
 XX  
 XX 01-JUL-2002; 2002US-0392382P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA;  
 XX  
 XX WPI; 2004-071976/07.  
 XX  
 XX N-PSDB; AD158113.  
 XX  
 XX Novel antibody, useful for treating, preventing or ameliorating  
 PT inflammatory bowel disorder, cancer of the gastrointestinal tract or  
 PT diabetes (non-insulin dependent diabetes or insulin dependent diabetes).  
 XX  
 XX  
 PS Claim 2; SEQ ID NO 6; 324bp; English.  
 XX  
 XX The invention comprises an antibody that specifically binds a  
 CC regeneration IV (Reg IV) protein. The invention specifically comprises  
 CC the amino acid and coding sequences of single chain antibody fragments  
 CC (scFv's) that bind Reg IV protein. The antibody of the invention is  
 CC useful for treating, preventing and ameliorating: inflammatory bowel  
 CC disorders (e.g. ulcerative colitis or Crohn's disease), diabetes (e.g.  
 CC non-insulin dependent diabetes or insulin dependent diabetes), and cancer  
 CC of the gastrointestinal tract. The antibody of the invention is also  
 CC useful for detecting the expression of a Reg IV protein. The present  
 CC amino acid sequence represents an scFv of the invention.  
 XX  
 XX Sequence 243 AA;  
 SQ  
 Query Match 83.0%; Score 1051.5; DB 8; Length 243;  
 Best Local Similarity 83.7%; Pred. No. 1e-66;  
 Matches 205; Conservative 14; Mismatches 21; Indels 5; Gaps 2;  
 QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPKGLEWVSISGSSRYYY 60  
 DB 1 EVQLVQSGGGLVQPGKSLRLSCAASGFTSSYGMHWVRAQPKGLEWVAIVISDGSKYY 60  
 QY 61 ADSVKGKFTISRDNKNTLYLQWNSLRADTAIVYCAKMDASGSY---FNFMGQGTLYTV 117  
 DB 61 ADSVKGKFTISRDNKNTLYLQWNSLRADTAIVYCAK--ASYYVFWFDINGCGIMTV 118  
 QY 118 SSGGGGGGGGGGGSETTLTQSPFSLAFAVGDRIITTCRASPGIRNYLAWYQKPKA 177  
 DB 119 SSGGGGGGGGGGGSGSDIQMTQSPSLASVADVITTCRASQGINNYLAWYQKPKA 178  
 QY 178 PKLLIYAASTLQSGVSRFGSGSGGCDPFLITISLQPPRPATYYCOQVNSYPLSPFGGK 237  
 DB 179 PKLLIYAASTLQSGVSRFGSGSGGTDFTLTISLQPPEDPATYYCLQSDSDYPLTFGGGK 238  
 QY 238 VEIKR 242  
 DB 239 LEIKR 243  
 RESULT 12  
 ABP45871  
 XX ID ABP45871 standard; protein; 239 AA.  
 AC ABP45871;  
 XX

DT 19-AUG-2002 (first entry)  
 XX  
 DE Human Blys binding scFv SEQ ID 1882.  
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200202641-A1.  
 XX  
 XX 10-JAN-2002.  
 XX  
 XX 15-JUN-2001; 2001WO-US019110.  
 XX  
 XX 16-JUN-2000; 2000US-0212210P.  
 XX  
 XX 17-OCT-2000; 2000US-0240816P.  
 XX  
 XX 16-MAR-2001; 2001US-0276248P.  
 XX  
 XX 21-MAR-2001; 2001US-0277379P.  
 XX  
 XX 25-MAY-2001; 2001US-0293499P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 PI  
 DR WPI; 2002-114799/15.  
 XX  
 XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.  
 PT  
 PS Claim 1; Page 2647-2648; 3148bp; English.  
 XX  
 XX This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antineumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention  
 XX  
 XX Sequence 239 AA;  
 SQ  
 Query Match 82.9%; Score 1050.5; DB 5; Length 239;  
 Best Local Similarity 81.8%; Pred. No. 1.2e-66;  
 Matches 198; Conservative 23; Mismatches 18; Indels 3; Gaps 1;  
 QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPKGLEWVSISGSSRYYY 60  
 DB 1 EVQLVQSGGGLVQPGKSLRLSCAASGFTSSYGMHWVRAQPKGLEWVAIVISDGSKYY 60  
 QY 61 ADSVKGKFTISRDNKNTLYLQWNSLRADTAIVYCAK---TSGSGFDVGRGTLYTVSSG 120  
 DB 61 ADSVKGKFTISRDNKNTLYLQWNSLRADTAIVYCAK--TSGSGFDVGRGTLYTVSSG 117  
 QY 121 GGGSGGGGGGGGGSETTLTQSPFSLAFAVGDRIITTCRASPGIRNYLAWYQKPKA 180  
 DB 118 GGGSGGGGGGGGGSGSDIQMTQSPSLASIGRVITTCRASPGIRNYLAWYQKPKA 177



CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS  
 CC and so may be used to detect and quantitate the presence of BlyS in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of BlyS. They may also be  
 CC administered to treat diseases associated with aberrant BlyS expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID), and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention

XX Sequence 248 AA;

Query Match 82.9%; Score 1050; DB 5; Length 248;  
 Best Local Similarity 80.6%; Pred. No. 1.4e-66;  
 Matches 200; Conservative 20; Mismatches 22; Indels 6; Gaps 1;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMGVROAPGKLEWVSSISGSRITY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMHVRQAPGKLEWVAVISYDGSNKYY 60  
 QY 61 ADSVKGRTFTISRDNKNTLYIQMNSLRADPTAVYYCAK-----MDASGSYENFMGQGT 114  
 DB 61 ADSVKGRTFTISRDNKNTLYIQMNSLRADPTAVYYCAKAYVDILTGYSYDYDWGKGT 120  
 QY 115 VTVSSGGGGGGGGGGSGSETTLTQSPFSLAFVGRITTCRASPGIRNLAWYQOKP 174  
 DB 121 VTVSSGGGGGGGGGGSGSETTLTQSPFSLAFVGRITTCRASPGIRNLAWYQOKP 180  
 QY 175 GKAPKLLIYASTLOSGLVPSRPSGSGGTDFLTITSSLOPEDFATYYCCQVNSYPLSFG 234  
 DB 181 GKAPKLLIYKASSLSAGAPSRPSGSGGTDFLTITSSLOPEDFATYYCCQVNSYPLTFFG 240  
 QY 235 GTKVEIKR 242  
 DB 241 GTKLEIKR 248

RESULT 15

ADG96237 standard; protein; 248 AA.

ADG96237;

11-MAR-2004 (first entry)

DE Single chain antibody that immunospecifically binds BlyS SeqID 1421.

KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;  
 KW B cell proliferation; differentiation; scfv; myasthenia gravis;  
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;  
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;  
 KW antiinflammatory; antiaesthetic; antiallergic; cytostatic.

XX Unidentified.

XX MO2003055979-A2.

XX 10-JUL-2003.

XX 14-NOV-2002; 2002WO-US036496.

XX 16-NOV-2001; 2001US-0331469P.

XX 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX WPI; 2003-505530/47.

PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
 PT (BlyS), useful for detecting and treating diseases or disorders e.g.  
 PT rheumatoid arthritis, asthma and leukemia.

PS Example 1; SEQ ID NO 1421; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind  
 CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to  
 CC chromosome 13q34 and encodes a protein that is a member of the tumour  
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
 CC proliferation and differentiation. Specifically, it refers to single  
 CC chain antibody molecules (scfvs) derived, preferably, from the variable  
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
 CC fragment thereof, of either human, murine, rat or monkey BlyS. The  
 CC present invention refers to the use of such antibodies in various methods  
 CC for the detection, diagnosis and prognosis of diseases related to the  
 CC aberrant expression or inappropriate function of BlyS or its receptor. As  
 CC such, these compositions are useful for identifying immune disorders  
 CC including myasthenia gravis and multiple sclerosis, inflammatory  
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
 CC lymphoma. Accordingly, they can be described as exhibiting various  
 CC activities such as antirheumatic, antiallergic and neuroprotective.  
 CC antiinflammatory, antiaesthetic, antiallergic and cytostatic. This  
 CC polypeptide sequence is a single chain antibody that binds BlyS of the  
 CC invention. NOTE: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 248 AA;

Query Match 82.9%; Score 1050; DB 7; Length 248;  
 Best Local Similarity 80.6%; Pred. No. 1.4e-66;  
 Matches 200; Conservative 20; Mismatches 22; Indels 6; Gaps 1;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMGVROAPGKLEWVSSISGSRITY 60  
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMHVRQAPGKLEWVAVISYDGSNKYY 60  
 QY 61 ADSVKGRTFTISRDNKNTLYIQMNSLRADPTAVYYCAK-----MDASGSYENFMGQGT 114  
 DB 61 ADSVKGRTFTISRDNKNTLYIQMNSLRADPTAVYYCAKAYVDILTGYSYDYDWGKGT 120  
 QY 115 VTVSSGGGGGGGGGGSGSETTLTQSPFSLAFVGRITTCRASPGIRNLAWYQOKP 174  
 DB 121 VTVSSGGGGGGGGGGSGSETTLTQSPFSLAFVGRITTCRASPGIRNLAWYQOKP 180  
 QY 175 GKAPKLLIYASTLOSGLVPSRPSGSGGTDFLTITSSLOPEDFATYYCCQVNSYPLSFG 234  
 DB 181 GKAPKLLIYKASSLSAGAPSRPSGSGGTDFLTITSSLOPEDFATYYCCQVNSYPLTFFG 240  
 QY 235 GTKVEIKR 242  
 DB 241 GTKLEIKR 248

Search completed: April 19, 2005, 16:39:13  
 Job time : 122.008 secs

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on: April 19, 2005, 16:32:47 ; Search time 29.7541 Seconds  
(without alignments)  
607.146 Million cell updates/sec

Title: US-09-250-056B-2

Perfect score: 1267  
Sequence: 1 QVQLVESGGGLVQPGGSLRL.....QQYNSTPLSPFGGTTKEIKR 242

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1057.5	83.5	245	US-09-138-091A-76	Sequence 76, Appl
2	1056.5	83.4	245	US-08-918-148-78	Sequence 78, Appl
3	1047	82.6	240	US-09-192-854-2	Sequence 2, Appl
4	1040.5	82.1	245	US-08-918-148-75	Sequence 75, Appl
5	1040.5	82.1	245	US-09-138-091A-73	Sequence 73, Appl
6	1002.5	79.1	245	US-08-918-148-76	Sequence 76, Appl
7	1002.5	79.1	245	US-09-138-091A-74	Sequence 74, Appl
8	1002	79.1	244	US-08-918-148-77	Sequence 77, Appl
9	1002	79.1	244	US-09-138-091A-75	Sequence 75, Appl
10	937.5	74.0	284	US-08-564-164A-2	Sequence 2, Appl
11	921	72.7	301	US-08-661-052-14	Sequence 14, Appl
12	921	72.7	301	US-09-188-082-14	Sequence 14, Appl
13	921	72.7	301	US-09-364-088-14	Sequence 14, Appl
14	921	72.7	301	US-09-102-716-14	Sequence 14, Appl
15	921	72.7	553	US-08-661-052-16	Sequence 16, Appl
16	921	72.7	553	US-09-188-082-16	Sequence 16, Appl
17	921	72.7	553	US-09-364-088-16	Sequence 16, Appl
18	921	72.7	553	US-09-102-716-16	Sequence 16, Appl
19	914.5	72.2	240	US-08-488-113B-148	Sequence 148, App
20	914.5	72.2	240	US-08-477-84B-148	Sequence 148, App
21	914.5	72.2	240	US-08-646-360-148	Sequence 148, App
22	914.5	72.2	240	US-08-839-765-148	Sequence 148, App
23	914.5	72.2	240	US-09-136-389-148	Sequence 148, App
24	914.5	72.2	240	US-09-610-838-148	Sequence 148, App
25	914.5	72.2	240	US-09-711-485-148	Sequence 148, App
26	912	72.0	248	US-08-887-352B-23	Sequence 23, Appl
27	912	72.0	248	US-09-109-207C-23	Sequence 23, Appl

28	912	72.0	248	US-09-296-005-23	Sequence 23, Appl
29	912	72.0	248	US-09-920-171-23	Sequence 23, Appl
30	912	72.0	248	US-09-716-028-23	Sequence 23, Appl
31	912	72.0	248	US-10-113-396-23	Sequence 23, Appl
32	911	71.9	248	US-08-887-352B-22	Sequence 22, Appl
33	911	71.9	248	US-09-109-207C-22	Sequence 22, Appl
34	911	71.9	248	US-09-296-005-22	Sequence 22, Appl
35	911	71.9	248	US-09-920-171-22	Sequence 22, Appl
36	911	71.9	248	US-09-716-028-22	Sequence 22, Appl
37	911	71.9	248	US-10-113-396-22	Sequence 22, Appl
38	909.5	71.8	281	US-09-025-768B-178	Sequence 178, App
39	909.5	71.8	281	US-09-490-070A-178	Sequence 178, App
40	909.5	71.8	281	US-09-490-153-178	Sequence 178, App
41	909.5	71.8	281	US-09-490-324-178	Sequence 178, App
42	893.5	70.5	282	US-08-860-174A-10	Sequence 10, Appl
43	884	69.8	236	US-08-190-199A-65	Sequence 65, Appl
44	873	68.9	255	US-09-553-498-8	Sequence 8, Appl
45	873	68.9	255	US-09-618-863-8	Sequence 8, Appl

## ALIGNMENTS

```
RESULT 1
US-09-138-091A-76
; Sequence 76, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian L.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
; CURRENT APPLICATION NUMBER: US/09/138,091A
; PRIOR FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: US 60/056,736
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: single chain antibody (scFv) fragments
; NAME/KEY: VARIANT
; LOCATION: 208
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-138-091A-76

Query Match      83.5%; Score 1057.5; DB 4; Length 245;
Best Local Similarity 83.1%; Pred. No. 2.4e-73;
Matches 201; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTPSYAMGVRAQPGKLEWVSISGSSRYYY 60
DB 3 QVQLVESGGGLVQPGGSLRLSCAASGFTPSYAMGVRAQPGKLEWVSISGSSRYYY 62
QY 61 ADSVKRFTISRDNKNTLYIQNLSLRADTAIVYCAKMDAGSYENFGQGLTVVSSG 120
DB 63 ADSVKRFTISRDNKNTLYIQNLSLRADTAIVYCAR-DRGSTGMDVWGRTLVVSSG 121
QY 121 GGGSGGGSGGGSGSETTLQSPFSLAFVGDRTITTCRASPGIRNLAVYQKRGAPYL 180
DB 122 GGGSGGGSGGGSGSDIQMTQSPSTLSASIGDRVITTCRASPGIRNLAVYQKRGAPYL 181
QY 181 LITRAASTLQGVPSRFGSGSGTDFLTITSSIQPEDPATYTCQQNSYPLSPFGGTTKEI 240
DB 182 LITKASLASGAPSRFGSGSGTDFLTITSSIQPEDPATYTCQQNSYPLSPFGGTTKEI 241
QY 241 KR 242
```

Db 242 KR 243

## RESULT 2

US-08-918-148-78  
Sequence 78, Application US/08918148A

Patent No. 6342220

GENERAL INFORMATION:  
APPLICANT: Adams, Camellia

APPLICANT: W. Carter, Paul J.

APPLICANT: Rendly, Brian M.

APPLICANT: Gurney, Austin L.

TITLE OF INVENTION: Agonist Antibodies

CURRENT APPLICATION NUMBER: US/08/918,148A

CURRENT FILING DATE: 1997-08-25

NUMBER OF SEQ ID NOS: 79

SEQ ID NO 78

LENGTH: 245

TYPE: PRT

ORGANISM: artificial

FEATURE:

NAME/KEY: unknown

LOCATION: 208

OTHER INFORMATION: unknown amino acid

US-08-918-148-78

Query Match 83.4%; Score 1056.5; DB 3; Length 245;  
Best Local Similarity 83.1%; Pred. No. 2.9e-73;  
Matches 201; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVSSGGLVQPGGSLRLSCAASGFTPSYAMGVRAQAPKGLEWVSISGSRRIYY 60

DB 3 QVQLVSSGGLVQPGGSLRLSCAASGFTPSYAMGVRAQAPKGLEWVSISGSRRIYY 62

QY 61 ADSVKGRTISRDNSKNTLYIQMNSLRADTAIVYCAKMDASGYFNFVGGTLVTVSSG 120

DB 63 ADSVKGRTISRDNSKNTLYIQMNSLRADTAIVYCAR--DRSGTMDVGRGTLVTVSSG 121

QY 121 GGGSGGGSGGGSETTLTQSPFLSAFVGDRIITTCRASPGIRNYLAWYQOKPKAPKL 180

DB 122 GGGSGGGSGGGSETTLTQSPFLSAFVGDRIITTCRASPGIRNYLAWYQOKPKAPKL 181

QY 181 LIYAASLTQSGVPSRPSGSGGTDFTLTISLQPEDPATYCCQYNSYPLSFGGKTVKEI 240

DB 182 LIYKASSLASGAPSRPSGSGGTDFTLTISLQPEDPATYCCQYNSYPLSFGGKTVKEI 241

QY 241 KR 242

DB 242 KR 243

## RESULT 3

US-09-192-854-2  
Sequence 2, Application US/09192854

Patent No. 6696245

GENERAL INFORMATION:  
APPLICANT: Winter, Greg

APPLICANT: Tomlinson, Ian

TITLE OF INVENTION: Methods for Selecting Functional Peptides

CURRENT APPLICATION NUMBER: US/09/192,854

EARLIER FILING DATE: 1998-11-17

NUMBER OF SEQ ID NOS: 212

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 240

TYPE: PRT

ORGANISM: Homo sapiens

US-09-192-854-2

Query Match 82.6%; Score 1047; DB 4; Length 240;  
Best Local Similarity 85.2%; Pred. No. 1.5e-72;  
Matches 207; Conservative 11; Mismatches 21; Indels 4; Gaps 2;

QY 1 QVQLVSSGGLVQPGGSLRLSCAASGFTPSYAMGVRAQAPKGLEWVSISGSRRIYY 60

DB 1 EVQLVSSGGLVQPGGSLRLSCAASGFTPSYAMGVRAQAPKGLEWVSISGSGSTYY 60

QY 61 ADSVKGRTISRDNSKNTLYIQMNSLRADTAIVYCAKMDASGYFNFVGGTLVTVSSG 120

DB 61 ADSVKGRTISRDNSKNTLYIQMNSLRADTAIVYCAR--SYGAFDHWGGTLVTVSSG 117

QY 121 GGGSGGGSGGGSETTLTQSPFLSAFVGDRIITTCRASPGIRNYLAWYQOKPKAPKL 179

DB 118 GGGSGGGSGGGSETTLTQSPFLSAFVGDRIITTCRASPGIRNYLAWYQOKPKAPKL 177

QY 180 LIYAASLTQSGVPSRPSGSGGTDFTLTISLQPEDPATYCCQYNSYPLSFGGKTVKEI 239

DB 178 LIYAASLTQSGVPSRPSGSGGTDFTLTISLQPEDPATYCCQYNSYPLSFGGKTVKEI 237

QY 240 IIR 242

DB 238 IIR 240

## RESULT 4

US-08-918-148-75  
Sequence 75, Application US/08918148A

Patent No. 6342220

GENERAL INFORMATION:  
APPLICANT: Adams, Camellia

APPLICANT: W. Carter, Paul J.

APPLICANT: Rendly, Brian M.

APPLICANT: Gurney, Austin L.

TITLE OF INVENTION: Agonist Antibodies

CURRENT APPLICATION NUMBER: US/08/918,148A

CURRENT FILING DATE: 1997-08-25

NUMBER OF SEQ ID NOS: 79

SEQ ID NO 75

LENGTH: 245

TYPE: PRT

ORGANISM: artificial

US-08-918-148-75

Query Match 82.1%; Score 1040.5; DB 3; Length 245;  
Best Local Similarity 81.0%; Pred. No. 4.8e-72;  
Matches 196; Conservative 20; Mismatches 25; Indels 1; Gaps 1;

QY 1 QVQLVSSGGLVQPGGSLRLSCAASGFTPSYAMGVRAQAPKGLEWVSISGSRRIYY 60

DB 3 EVQLVSSGGLVQPGGSLRLSCAASGFTPSYAMGVRAQAPKGLEWVSISGSGSTYY 62

QY 61 ADSVKGRTISRDNSKNTLYIQMNSLRADTAIVYCAKMDASGYFNFVGGTLVTVSSG 120

DB 63 ADSVKGRTISRDNSKNTLYIQMNSLRADTAIVYCARMSGDA--FDIKGGCTVTVSSG 121

QY 121 GGGSGGGSGGGSETTLTQSPFLSAFVGDRIITTCRASPGIRNYLAWYQOKPKAPKL 180

DB 122 GGGSGGGSGGGSETTLTQSPFLSAFVGDRIITTCRASPGIRNYLAWYQOKPKAPKL 181

QY 181 LIYAASLTQSGVPSRPSGSGGTDFTLTISLQPEDPATYCCQYNSYPLSFGGKTVKEI 240

DB 182 LIYKASSLASGAPSRPSGSGGTDFTLTISLQPEDPATYCCQYNSYPLSFGGKTVKEI 241

QY 241 KR 242

DB 242 KR 243



```

RESULT 5
US-09-118-091A-73
; Sequence 73, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Pendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
; CURRENT APPLICATION NUMBER: US/09/138,091A
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: US 60/056,736
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: single chain antibody (scFv) fragments
US-09-138-091A-73

Query Match      82.1%; Score 1040.5; DB 4; Length 245;
Best Local Similarity 81.0%; Pred. No. 4,8e-72;
Matches 196; Conservative 20; Mismatches 25; Indels 1; Gaps 1;

OY    1 QVALVESGGLVQPGSGSLRLSCAAAGFPSSSYAMGMVRQAPEGLEWYSISGSRRYYI 60
Db    3 EVOLVOSGGGLVKPGGSRRLSCAASGFITFDYIMKIROAPEKGLEWYSISSGSTIYY 62
OY    61 ADVXGREFTISRDN SKNTLYIQMNSLRABEDTA VVYCANKMDASGYFNFGQTIVTVS 120
Db    63 ADVXGREFTISRDN SKNTLYIQMNSLRABEDTA VVYCANKMSGEDA-FDLMGGTIVTVS 121
OY    121 GGGSGGGSGGGSGSTTTLTGSPFLSARVGDRIITTCASPDIRNYALAMYQQPKAPKL 180
Db    122 GGGSGGGSGGGSGSDIIVWTOSPSTLSASVGDRVAITCAASEGIYHMLAWYQQPKAPKL 181
OY    181 LIYAASTLQGVAPRPFSGSGSGTDPTLTITSSLOPEDFAITYCCQYNVPLSRFGGTXYEI 240
Db    182 LIYKASSLASGAPSRPFSGSGADPTLTITSSLOPDPAFYICQYQSNYPILTFGGTKLEV 241
OY    241 KR 242
Db    242 KR 243

RESULT 6
US-08-918-148-76
; Sequence 76, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Pendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 76
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial
US-08-918-148-76

Query Match      79.1%; Score 1002.5; DB 3; Length 245;
Best Local Similarity 79.0%; Pred. No. 3,8e-69;

```

Matches	192;	Conservative	21;	Mismatches	27;	Indels	3;	Gaps	2
QY	1	QVVLVESGGGGLVPOGGGSLRLSCAASGFFPSYAMGWROAPKGLEWVSSISGSSRYYY	60						
Db	3	EVOLVOSGGGVQPGGSSLSLSCAVSGITLRTYGMHWROAPGKLEWVAGISFDGRSEYY	62						
QY	61	ADSVKGRFTISRDNKNTLYIQNMNSLRAPEDPAVYYCAKMDASGY-FNFMQGTLLVTSS	119						
Db	63	ADSVKGRFTISRDNKNTLYIQNMNSLRAPEDPAVYYCAR--DRGSYGMQVWGRGTWTVSS	120						
QY	120	GGGSGGGGGSGGGSETTLTQSPFSLAPVADRITITCRASPGIRNYLAWYQOKRKAPK	179						
Db	121	GGGSGGGGGSGGGSDIQMTQSPFTLSASIDRVITITCRASPGIRNYLAWYQOKRKAPK	180						
QY	180	LLIYAASLTQSGVSRPSGSGSGDTFTLTSSLOPEDPATYYCOQYNSYPLSPFGGCTVE	239						
Db	181	LLIYKASSLASGAPSRFSGSGSGDTFTLTSSLOPDPAIYYCOQYNSYPLPFGGCTYLE	240						
QY	240	IKR 242							
Db	241	ILR 243							
RESULT 7									
	US-09-138-091A-74								
	Sequence 74, Application US/09138091A								
	Patent No. 6737249								
	GENERAL INFORMATION:								
	APPLICANT: Adams, Camellia W.								
	APPLICANT: Carter, Paul J.								
	APPLICANT: Fendley, Brian M.								
	APPLICANT: Gurney, Austin L.								
	TITLE OF INVENTION: Agonist Antibodies								
	FILE REFERENCE: 9491-013-27								
	CURRENT APPLICATION NUMBER: US/09/138, 091A								
	CURRENT FILING DATE: 1998-08-21								
	PRIOR APPLICATION NUMBER: US 60/056, 736								
	PRIOR FILING DATE: 1997-08-22								
	NUMBER OF SEQ ID NOS: 77								
	SOFTWARE: FastSeq for Windows Version 4.0								
	SEQ ID NO 74								
	LENGTH: 245								
	TYPE: PRT								
	ORGANISM: Artificial Sequence								
	FEATURES:								
	OTHER INFORMATION: single chain antibody (scFv) fragments								
	US-09-138-091A-74								
Query Match	79.1%;	Score 1002.5;	DB 4;	Length 245;					
Best Local Similarity	79.0%;	Pred. No. 3.8e-69;							
Matches 192;	Conservative 21;	Mismatches 27;	Indels 3;	Gaps 2;					
QY	1	QVVLVESGGGGLVPOGGGSLRLSCAASGFFPSYAMGWROAPKGLEWVSSISGSSRYYY	60						
Db	3	EVOLVOSGGGVQPGGSSLSLSCAVSGITLRTYGMHWROAPGKLEWVAGISFDGRSEYY	62						
QY	61	ADSVKGRFTISRDNKNTLYIQNMNSLRAPEDPAVYYCAKMDASGY-FNFMQGTLLVTSS	119						
Db	63	ADSVKGRFTISRDNKNTLYIQNMNSLRAPEDPAVYYCAR--DRGSYGMQVWGRGTWTVSS	120						
QY	120	GGGSGGGGGSGGGSETTLTQSPFSLAPVADRITITCRASPGIRNYLAWYQOKRKAPK	179						
Db	121	GGGSGGGGGSGGGSDIQMTQSPFTLSASIDRVITITCRASPGIRNYLAWYQOKRKAPK	180						
QY	180	LLIYAASLTQSGVSRPSGSGSGDTFTLTSSLOPEDPATYYCOQYNSYPLSPFGGCTVE	239						
Db	181	LLIYKASSLASGAPSRFSGSGSGDTFTLTSSLOPDPAIYYCOQYNSYPLPFGGCTYLE	240						
QY	240	IKR 242							
Db	241	ILR 243							

Query Match	79.1%;	Score 1002;	DB 4;	Length 244;
Best Local Similarity	77.9%;	Pred. No. 4.1e-69;		

Query Match	74.0%;	Score 937.5;	DB 3;	Length 284;
Best Local Similarity	71.2%;	Pred. NO. 4e-64;		
Matches 173;	Conservative 32;	Mismatches 37;	Indels 1;	Gaps 1.

Db	22	IQLVSGGGVAVPGRSLRLSCSSGCFIPSDNYMMVWRQAPKGLMEVATISDGSITYYP	80
QY	62	DSYKRFITSRNRSKNTLLYLQMSLRADPTAVYCAKMDASGY-----FNFQGCGLVT	116
Db	81	DSYKRFITSRNRSKNTLLFLQMDSLRPEDTVYFCAR---GYRRYGAMDVQGGIPVT	136
QY	117	VSSGGGGSGGGSGGGSEITLTQSPSLSAFVGGDIRITTCRASPGI-----RNYLAMY	170
Db	137	VSSGGGGSGGGSGGGSGGSDIQLTQSPSLSAFVGGDIRVITTCSSQSYLVSSNQNYLAMY	196
QY	171	QQKPKGAPKLLIYAASLTQGYVPSRFSSGSGTDFTLTISSLQPEDPATIYCCQYNISYPL	230
Db	197	QQKPKGAPKLLIYMASTRSGVPSRFSSGSGTDFTLTISLQPEDIATYCYHQYLS-SW	255
QY	231	SFGGATKVEIK	241
Db	256	TFGGATKVEIK	266

```

1      RESULT 12
2      US-09-188-082-14
3      Sequence 14, Application US/09188082
4      Patent No. 6270765
5      GENERAL INFORMATION:
6      APPLICANT: Yashwant M. Deo
7      APPLICANT: Joel Goldstein
8      APPLICANT: Robert Graziano
9      APPLICANT: Chezian Somasundaram
10     TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
11     TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
12     NUMBER OF SEQUENCES: 16
13     CORRESPONDENCE ADDRESS:
14     ADDRESSEE: LAHIVE & COCKFIELD
15     STREET: 60 State Street, Suite 510
16     City: Boston
17     STATE: Massachusetts
18     COUNTRY: USA
19     ZIP: 02109-1875
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Floppy disk
22     COMPUTER: IBM PC compatible
23     OPERATING SYSTEM: PC-DOS/MS-DOS
24     SOFTWARE: PatentIn Release #1.0, Version #1.25
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/09/188,082
27     FILING DATE:
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: 08/661,052
30     FILING DATE:
31     ATTORNEY/AGENT INFORMATION:
32     NAME: Arnold, Beth E.
33     REGISTRATION NUMBER: 35,430
34     REFERENCE/DOCKET NUMBER: MX1-043CP
35     TELECOMMUNICATION INFORMATION:
36     TELEPHONE: (617)227-7400
37     TELEFAX: (617)227-5941
38     INFORMATION FOR SEQ ID NO: 14:
39     SEQUENCE CHARACTERISTICS:
40     LENGTH: 301 amino acids
41     TYPE: amino acid
42     TOPOLOGY: linear
43     MOLECULE TYPE: protein
44     US-09-188-082-14

```

```
. Query Match      72.7%; Score 92; DB 3; Length 301;
Best Local Similarity 72.9%; P-Ed. 7.8e-63;
Matches 183; Conservative 20; Mismatches 32; Indels 16; Gaps 4

QY      2 VQLVGGGGLNPGSGILRLSCAAGPTTSSVYMGMVRAPKGGLEWVSISGSRYIYA 61
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      21 IQLVGGGGLNPGSKRLSLRSCSSGFIISDNMTMYRRAPKGLEWATIEDGSIYYIP 80

QY      62 DSVKGFITSRDNSKTLLYLQNNLSLRAEDTAVIYCAKDADGASY-----RFPMQGCLVT 116
```

Db 81 DSVKGFRTISRNSKNTLFLQMDSLRPEDTGVYFCAR-----GYRYEGAMDYWGQTPVT 136  
QY 117 VSSGGGGGGGGGGGGGGSETTLTOSPSFLSAFVGDRITTTCCASPCI-----RNYLAMY 170  
137 VSSGGGGGGGGGGGGGGSDIQLTQSPSSLSASVGDRTVITCKSSQSVLYSSNQKNYLA 196  
Db 171 OOKPGKAPKLLIYAASLTOSGVPSPRSFGSGGSDTFTLTITSSLOPPDPATYYCOQYNSYPL 230  
197 OOKPGKAPKLLIYMASTRSGVSPRSFGSGGSDTFTFTITSSLOPPDIATYYCHQYLS-SW 255  
QY 231 SFGGKTKEIK 241  
Db 256 TFGGKTKEIK 266

RESULT 13  
US-09-364-088-14

/ Sequence 14, Application US/09364088  
/ Patent No. 6365161  
/ GENERAL INFORMATION:  
/ APPLICANT: Yashwant M. Deo, et al.  
/ TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
/ OF ANTI-FC RECEPTOR ANTIBODIES  
/ NUMBER OF SEQUENCES: 16  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: LAHIVE & COCKFIELD, LLP  
/ STREET: 28 State Street, 24th Floor  
/ CITY: Boston  
/ STATE: Massachusetts  
/ COUNTRY: USA  
/ ZIP: 02109  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ OPERATING SYSTEM: IBM PC compatible  
/ SOFTWARE: Patentin Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/364,088  
/ FILING DATE:  
/ PRIORITY APPLICATION DATA:  
/ APPLICATION NUMBER: US 09/188,082  
/ FILING DATE: 07-JUNE-1996  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/484,172  
/ FILING DATE: 07-JUNE-1995  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Remillard, Jane E.  
/ REGISTRATION NUMBER: 38,872  
/ REFERENCE/DOCKET NUMBER: MXI-043CP2  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (617)227-7400  
/ TELEFAX: (617)742-7414  
/ INFORMATION FOR SEQ ID NO: 14:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 301 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ US-09-364-088-14

Query Match 72.7%; Score 921; DB 3; Length 301;  
Best Local Similarity 72.9%; Pred. No. 7.8e-63;  
Matches 183; Conservative 20; Mismatches 32; Indels 16; Gaps 4;  
QY 2 VOLVESGGGLVPGGSLRLSLSAASGFTFSYAMGWROAPGKGLEWVSSISGSRITYYA 61  
1 IOLVESGGGVVPGSLRLSSSSGFIISDNTMYWYRQAPGKLEWVATISDGSSTYYP 80  
Db 21 IOLVESGGGVVPGSLRLSSSSGFIISDNTMYWYRQAPGKLEWVATISDGSSTYYP 80  
QY 62 DSVKGRFTISRNSKNTLFLQMDSLRPEDTGVYFCAR-----GYRYEGAMDYWGQTPVT 116  
Db 81 DSVKGRFTISRNSKNTLFLQMDSLRPEDTGVYFCAR-----GYRYEGAMDYWGQTPVT 136

QY 117 VSSGGGGGGGGGGGGGGSETTLTOSPSFLSAFVGDRITTTCCASPCI-----RNYLAMY 170  
137 VSSGGGGGGGGGGGGGGSDIQLTQSPSSLSASVGDRTVITCKSSQSVLYSSNQKNYLA 196  
Db 171 OOKPGKAPKLLIYAASLTOSGVPSPRSFGSGGSDTFTLTITSSLOPPDPATYYCOQYNSYPL 230  
197 OOKPGKAPKLLIYMASTRSGVSPRSFGSGGSDTFTFTITSSLOPPDIATYYCHQYLS-SW 255  
QY 231 SFGGKTKEIK 241  
Db 256 TFGGKTKEIK 266

RESULT 14  
US-09-102-716-14

/ Sequence 14, Application US/09102716  
/ Patent No. 6395272  
/ GENERAL INFORMATION:  
/ APPLICANT: Yashwant M. Deo  
/ Robert Graziano  
/ Joel Goldstein  
/ Chehian Somaundaram  
/ TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
/ OF ANTI-FC RECEPTOR ANTIBODIES  
/ NUMBER OF SEQUENCES: 16  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: LAHIVE & COCKFIELD  
/ STREET: 60 State Street, Suite 510  
/ CITY: Boston  
/ STATE: Massachusetts  
/ COUNTRY: USA  
/ ZIP: 02109-1875  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ OPERATING SYSTEM: IBM PC compatible  
/ SOFTWARE: Patentin Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/102,716  
/ FILING DATE: 22-Jun-1998  
/ PRIORITY APPLICATION DATA:  
/ APPLICATION NUMBER: 08/661,052  
/ FILING DATE: <Unknown>  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Arnold, Beth E.  
/ REGISTRATION NUMBER: 35,430  
/ REFERENCE/DOCKET NUMBER: MXI-043CP  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (617)227-7400  
/ TELEFAX: (617)227-5941  
/ INFORMATION FOR SEQ ID NO: 14:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 301 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
/ US-09-102-716-14

Query Match 72.7%; Score 921; DB 3; Length 301;  
Best Local Similarity 72.9%; Pred. No. 7.8e-63;  
Matches 183; Conservative 20; Mismatches 32; Indels 16; Gaps 4;  
QY 2 VOLVESGGGLVPGGSLRLSLSAASGFTFSYAMGWROAPGKGLEWVSSISGSRITYYA 61  
1 IOLVESGGGVVPGSLRLSSSSGFIISDNTMYWYRQAPGKLEWVATISDGSSTYYP 80  
Db 21 IOLVESGGGVVPGSLRLSSSSGFIISDNTMYWYRQAPGKLEWVATISDGSSTYYP 80  
QY 62 DSVKGRFTISRNSKNTLFLQMDSLRPEDTGVYFCAR-----GYRYEGAMDYWGQTPVT 116  
Db 81 DSVKGRFTISRNSKNTLFLQMDSLRPEDTGVYFCAR-----GYRYEGAMDYWGQTPVT 136  
QY 117 VSSGGGGGGGGGGGGGGSETTLTOSPSFLSAFVGDRITTTCCASPCI-----RNYLAMY 170

Db 137 VSSGGGGGGGGGGSDIQLTQSPSSLSASVGDRTTTCSSQSVLYSSNOKNYLAWY 196  
QY 171 QOKPGKAPKLLIYAASLTQSGVPSRPSGSGGTDFLTITSLQPEDFATYCCOYNSYPL 230  
Db 197 QOKPGKAPKLLIYMASTRSGVPSRPSGSGGTDFLTITSLQPEDIATYCHQYLS-SW 255  
QY 231 SFGGKTKVEIK 241  
Db 256 TFGGKTKVEIK 266

## RESULT 15

US-08-661-052-16  
Sequence 16, Application US/08661052  
Patent No. 5837243  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo  
APPLICANT: Joel Goldstein  
APPLICANT: Robert Graziano  
APPLICANT: Chezian Somasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,052  
FILING DATE:  
Prior Application DATA:  
APPLICATION NUMBER: US 08/484,172  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-661-052-16

Query Match 72.7%; Score 921; DB 2; Length 553;

Best Local Similarity 72.9%; Pred. No. 1.5e-62; Indels 16; Gaps 4;  
Matches 183; Conservative 20; Mismatches 32;

QY 2 VOLVESGGGLVDPGSLRLSCAAGFTFSYANGWVROAPGKLEWVSSISGSSRYIYYA 61  
Db 21 IQLVESGGGVVQGRSLRLSCSSGFLFSDNVMYWRQAPGKLEWVATISDGSYTYIP 80  
QY 62 DSVKGRFTISRDNKSTLYIQMNSLRPAEDTAVYICAMDAAGSY-----FNFWGGTLVT 116  
Db 81 DSVKGRFTISRDNKSTLYIQMNSLRPAEDTAVYICAMDAAGSY-----GYRYEGAMDYWGQGPVT 136  
QY 117 VSSGGGGGGGGGGGGSETTLTQSPFLSAFVGDRTTTCRASPGI-----RNYLAWY 170  
Db 137 VSSGGGGGGGGGGGGSDIQLTQSPSSLSASVGDRTTTCSSQSVLYSSNOKNYLAWY 196  
QY 171 QOKPGKAPKLLIYAASLTQSGVPSRPSGSGGTDFLTITSLQPEDFATYCCOYNSYPL 230

Db 197 QOKPGKAPKLLIYMASTRSGVPSRPSGSGGTDFLTITSLQPEDIATYCHQYLS-SW 255  
QY 231 SFGGKTKVEIK 241  
Db 256 TFGGKTKVEIK 266

Search completed: April 19, 2005, 16:45:20  
Job time : 30.7541 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2005, 16:43:24 ; Search time 87.2787 Seconds  
(without alignments)  
921.573 Million cell updates/sec

Title: US-09-250-056B-2

Perfect score: 1267  
Sequence: 1 QVQLVSGGGLVQPGGSLRL.....QQNSYPLSGFGGKTVEIKR 242

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1267	100.0	242	17	US-10-855-755-2 Sequence 2, Appl1
2	1084.5	85.6	239	17	US-10-935-290-80 Sequence 10, Appl1
3	1069	84.4	291	15	US-10-406-830-10 Sequence 80, Appl1
4	1065.5	84.1	288	9	US-09-818-247-22 Sequence 22, Appl1
5	1060.5	83.7	247	10	US-09-880-748-1923 Sequence 1923, Ap
6	1060.5	83.7	247	15	US-10-293-418-1923 Sequence 1923, Ap
7	1058.5	83.5	239	10	US-09-880-748-1922 Sequence 1922, Ap
8	1058.5	83.5	239	15	US-10-293-418-1922 Sequence 1922, Ap
9	1050.5	82.9	239	10	US-09-880-748-1882 Sequence 1882, Ap
10	1050.5	82.9	239	15	US-10-293-418-1882 Sequence 1882, Ap
11	1050	82.9	248	10	US-09-880-748-1421 Sequence 1421, Ap
12	1050	82.9	248	15	US-10-293-418-1421 Sequence 1421, Ap
13	1047	82.6	240	9	US-09-192-854-2 Sequence 2, Appl1

14	1047	82.6	240	9	US-09-968-561A-2	Sequence 2, Appl1
15	1047	82.6	240	10	US-09-968-744A-2	Sequence 2, Appl1
16	1047	82.6	240	11	US-09-968-561A-2	Sequence 12, Appl1
17	1046	82.6	250	15	US-10-423-847-12	Sequence 12, Appl1
18	1046	82.6	250	17	US-10-831-063-12	Sequence 98, Appl1
19	1044	82.4	240	17	US-10-935-290-98	Sequence 1935, Ap
20	1043.5	82.4	243	10	US-09-880-748-1935	Sequence 1935, Ap
21	1043.5	82.4	243	15	US-10-293-418-1935	Sequence 16, Appl1
22	1041	82.2	249	15	US-10-423-847-16	Sequence 15, Appl1
23	1041	82.2	249	17	US-10-831-063-16	Sequence 15, Appl1
24	1041	82.2	250	15	US-10-423-847-15	Sequence 15, Appl1
25	1041	82.2	250	17	US-10-831-063-15	Sequence 15, Appl1
26	1040.5	82.1	251	10	US-09-880-748-1910	Sequence 1310, Ap
27	1040.5	82.1	251	15	US-10-293-418-1310	Sequence 50, Appl1
28	1040	82.1	241	8	US-08-779-457-50	Sequence 9, Appl1
29	1040	82.1	241	17	US-10-921-710-50	Sequence 1945, Ap
30	1039	82.0	291	15	US-10-406-830-9	Sequence 82, Appl1
31	1033.5	81.6	243	10	US-09-880-748-1945	Sequence 2005, Ap
32	1033.5	81.6	243	15	US-10-293-418-1945	Sequence 1889, Ap
33	1031	81.4	244	10	US-09-880-748-82	Sequence 1901, Ap
34	1031	81.4	244	15	US-10-293-418-82	Sequence 1889, Ap
35	1029.5	81.3	237	10	US-09-880-748-2005	Sequence 1177, Ap
36	1029.5	81.3	237	15	US-10-293-418-2005	Sequence 2005, Ap
37	1029.5	81.3	241	10	US-09-880-748-1889	Sequence 1889, Ap
38	1029.5	81.3	241	15	US-09-880-748-1889	Sequence 1901, Ap
39	1029.5	81.3	241	10	US-10-293-418-1889	Sequence 1889, Ap
40	1029.5	81.3	241	15	US-10-293-418-1889	Sequence 1177, Ap
41	1029.5	81.3	247	10	US-09-880-748-1177	Sequence 1177, Ap
42	1029.5	81.3	247	15	US-10-293-418-1177	Sequence 1177, Ap
43	1027.5	81.1	237	10	US-09-880-748-2114	Sequence 2114, Ap
44	1027.5	81.1	237	15	US-10-293-418-2114	Sequence 2114, Ap
45	1027	81.1	244	10	US-09-880-748-164	Sequence 164, App

## ALIGNMENTS

RESULT 1  
US-10-855-755-2  
Sequence 2, Application US/10855755  
Publication No. US20050037339A1  
GENERAL INFORMATION:  
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
APPLICANT: Marks, James D  
APPLICANT: Poul, Marie A  
APPLICANT: Becerril, Balazar  
TITLE OF INVENTION: METHODS OF SELECTING INTERNALIZING ANTIBODIES  
FILE REFERENCE: 4070-895011US  
CURRENT APPLICATION NUMBER: US/10/855,755  
CURRENT FILING DATE: 2004-05-26  
PRIOR APPLICATION NUMBER: US 60/082,953  
PRIOR FILING DATE: 1998-04-24  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2  
LENGTH: 242  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Human phage display antibody  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (31)..(35)  
OTHER INFORMATION: VH-CDR1  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (50)..(66)  
OTHER INFORMATION: VH-CDR2  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (99)..(108)  
OTHER INFORMATION: VH-CDR3  
FEATURE:

NAME/KEY: SITE  
LOCATION: (157)..(167)  
OTHER INFORMATION: VL-CDR1  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (184)..(190)  
OTHER INFORMATION: VL-CDR2  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (223)..(231)  
OTHER INFORMATION: VL-CDR3  
US-10-855-755-2

Query Match 100.0%; Score 1267; DB 17; Length 242;  
Best Local Similarity 100.0%; Pred. No. 6.4e-79;  
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPGKLEWSSISGSSRYYY 60  
DB 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPGKLEWSSISGSSRYYY 60  
QY 61 ADSVGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKADASGSYFNFGQGLTVTVSSG 120  
DB 61 ADSVGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKADASGSYFNFGQGLTVTVSSG 120  
QY 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 180  
DB 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 180  
QY 181 LIYAASSTLOSQVPSRFSGSGSDTFTLTISLQPEDFATYYCOQYNSYPLSFGGKTVEI 240  
DB 181 LIYAASSTLOSQVPSRFSGSGSDTFTLTISLQPEDFATYYCOQYNSYPLSFGGKTVEI 240  
QY 241 KR 242  
DB 241 KR 242

## RESULT 2

US-10-935-290-80  
Sequence 80, Application US/10935290  
Publication No. US20050069542A1  
GENERAL INFORMATION:  
APPLICANT: Baker et al.  
FILE REFERENCE: PFS84Pl  
TITLE OF INVENTION: Antibodies that Specifically Bind to GMAD  
CURRENT APPLICATION NUMBER: US/10/935,290  
PRIOR FILING DATE: 2004-09-08  
PRIOR APPLICATION NUMBER: PCT/US03/09625  
PRIOR FILING DATE: 2003-03-28  
PRIOR APPLICATION NUMBER: 60/368,813  
NUMBER OF SEQ ID NOS: 234  
SEQ ID NO 80  
LENGTH: 239  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: scfv protein GMBG655  
US-10-935-290-80

Query Match 85.6%; Score 1084.5; DB 17; Length 239;  
Best Local Similarity 85.1%; Pred. No. 1.8e-66;  
Matches 206; Conservative 16; Mismatches 17; Indels 3; Gaps 1;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPGKLEWSSISGSSRYYY 60  
DB 1 EVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPGKLEWSSISGSSRYYY 60  
QY 61 ADSVGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKADASGSYFNFGQGLTVTVSSG 120  
DB 61 ADSVGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKADASGSYFNFGQGLTVTVSSG 120

QY 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 180  
DB 118 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 177  
QY 181 LIYAASSTLOSQVPSRFSGSGSDTFTLTISLQPEDFATYYCOQYNSYPLSFGGKTVEI 240  
DB 178 LIYAASSTLOSQVPSRFSGSGSDTFTLTISLQPEDFATYYCOQYNSYPLSFGGKTVEI 237  
QY 241 KR 242  
DB 238 KR 239

## RESULT 3

US-10-406-830-10  
Sequence 10, Application US/10406830  
Publication No. US20040071696A1  
GENERAL INFORMATION:  
APPLICANT: ADAMS, GREGORY P.  
APPLICANT: HORAK, EVA M.  
APPLICANT: WEINER, LOUIS M.  
APPLICANT: JAMES, MARKS D.  
TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
FILE REFERENCE: 407T-000410US  
CURRENT APPLICATION NUMBER: US/10/406,830  
PRIOR FILING DATE: 2003-04-04  
PRIOR APPLICATION NUMBER: US 60/370,276  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 10  
LENGTH: 291  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic antibody.  
US-10-406-830-10

Query Match 84.4%; Score 1069; DB 15; Length 291;  
Best Local Similarity 84.1%; Pred. No. 2.4e-65;  
Matches 207; Conservative 13; Mismatches 22; Indels 4; Gaps 1;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPGKLEWSSISGSSRYYY 60  
DB 23 QVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPGKLEWSSISGSSRYYY 82  
QY 61 ADSVGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKADASGSYFNFGQGLTVTVSSG 116  
DB 83 ADSVGRFTISRDNKNTLYLQMNSLRAEDTAVYCAKADASGSYFNFGQGLTVTVSSG 142  
QY 117 VSSGGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGK 176  
DB 143 VSSGGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGK 202  
QY 177 APLKLIYAASSTLOSQVPSRFSGSGSDTFTLTISLQPEDFATYYCOQYNSYPLSFGGKT 236  
DB 203 APLKLIYAASSTLOSQVPSRFSGSGSDTFTLTISLQPEDFATYYCOQYNSYPLSFGGKT 262  
QY 237 KVEIKR 242  
DB 263 KVEIKR 268

## RESULT 4

US-09-818-247-22  
Sequence 22, Application US/09818247  
Patent No. US20020102657A1  
GENERAL INFORMATION:  
APPLICANT: Mostoy, Keith E.  
APPLICANT: Chapin, Steven J.  
APPLICANT: Richman-Eisenstat, Janice  
APPLICANT: The Regents of the University of California



TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Secretory Component,  
FILE REFERENCE: No. US20020102657A1-Stralk Region of p19R and Methods of Use Ther  
CURRENT APPLICATION NUMBER: US/09/818,247  
CURRENT FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: WO PCT/US01/09699  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: US 60/192,197  
PRIOR FILING DATE: 2000-03-27  
PRIOR APPLICATION NUMBER: US 60/192,198  
PRIOR FILING DATE: 2000-03-27  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22  
LENGTH: 288  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial  
OTHER INFORMATION: Sequence: pelb/4AF/myc/6HIS  
US-09-818-247-22

Query Match 84.1%; Score 1065.5; DB 9; Length 288;  
Best Local Similarity 84.8%; Pred. No. 4.1e-65;  
Matches 206; Conservative 12; Mismatches 24; Indels 1; Gaps 1;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSVAMGVRAQPGKLEWVSISGSSRYYY 60  
DB 23 QVQLVSGGGLVQPGGSLRLSCAASGFTSSVAMGVRAQPGKLEWVSISGSSRYYY 82  
QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAK-MDASGYFNFVWGQGLTVVSS 119  
DB 83 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAKSTVNSGFGFHGQGLTVVSS 142  
QY 120 GGGSGGGSGGGSGGSETTLTQSPFLSAFVGDRITTTCPASPGIRNYLAWYQOKPG 179  
DB 143 GGGSGGGSGGGSGGSEIVLTQSPSTLSASIGDRVITTCASGSIYHMLAWYQOKPG 202  
QY 180 LIIYVASTQSGVPSRFSGSGGTDTLTISLQPEDPATYVYCOQNSYPLSGGTYYE 239  
DB 203 LIIYKASSLASGVPSPFSGSGGTDTLTISLQPEDPATYVYCOQNSYPLSGGTYYE 262  
QY 240 IKR 242  
DB 263 IKR 265

## RESULT 5

US-09-880-748-1923  
; Sequence 1923, Application US/09880748  
; Publication No. US2003005937A1  
GENERAL INFORMATION:  
; APPLICANT: Ruden et al.  
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind BlyS  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1923  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens

## US-09-880-748-1923

Query Match 83.7%; Score 1060.5; DB 10; Length 247;  
Best Local Similarity 82.2%; Pred. No. 7.8e-65;  
Matches 203; Conservative 20; Mismatches 19; Indels 5; Gaps 2;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSVAMGVRAQPGKLEWVSISGSSRYYY 60  
DB 1 EVQLVSGGGLVQPGGSLRLSCAASGFTSSVAMGVRAQPGKLEWVSISGSSRYYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAKMDA---SGS--YFNFGGGLV 115  
DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAKGNPRSSLYVFDWGRRTV 120  
QY 116 TVSSGGSGGGSGGSGSETTLTQSPFLSAFVGDRITTTCPASPGIRNYLAWYQOKPG 175  
DB 121 TVSSGGSGGGSGGSGSDIQNTQSPFLSASIGDRVITTCASGCIYHRLAWYQOKPG 180  
QY 176 KAPKLLIYVASTQSGVPSRFSGSGGTDTLTISLQPEDPATYVYCOQNSYPLSGGT 235  
DB 181 KAPKLLIYKASSLASGAPSPFSGSGGTDTLTISLQPEDPATYVYCOQNSYPLSGGT 240  
QY 236 TKYETIKR 242  
DB 241 TKLTIKR 247

## RESULT 6

US-10-293-418-1923  
; Sequence 1923, Application US/10293418  
; Publication No. US20030223996A1  
GENERAL INFORMATION:  
; APPLICANT: Ruden et al.  
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind BlyS  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1923  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-1923

Query Match 83.7%; Score 1060.5; DB 15; Length 247;  
Best Local Similarity 82.2%; Pred. No. 7.8e-65;  
Matches 203; Conservative 20; Mismatches 19; Indels 5; Gaps 2;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSVAMGVRAQPGKLEWVSISGSSRYYY 60  
DB 1 EVQLVSGGGLVQPGGSLRLSCAASGFTSSVAMGVRAQPGKLEWVSISGSSRYYY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAKMDA---SGS--YFNFGGGLV 115  
DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAKGNPRSSLYVFDWGRRTV 120  
QY 116 TVSSGGSGGGSGGSGSETTLTQSPFLSAFVGDRITTTCPASPGIRNYLAWYQOKPG 175

```

Db      121 TWSGGGGGGGGGGSDIQMTQSPSTLSASIGRVTTCRASGTHRLAMVQOKPG 180
Qy      176 KAPKLIIYAATLQSGVPSRFGSGSGTDFTLTISLQPEDPATYVCCQYNSYPLSPFGG 235
Db      181 KAPKLIVYKASSLASGAPSRFGSGSGTDFTLTISLQDPDFATYVCCQYNSYPLSPFGG 240
Qy      236 TVEIKR 242
Db      241 TKLTKR 247

RESULT 7
US-09-880-748-1922
; Sequence 1922, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; SOFTWARE OF SEQ ID NOS: 3239
; LENGTH: 239
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-880-748-1922

Query Match      83.5%; Score 1058.5; DB 10; Length 239;
Best Local Similarity 83.5%; Pred. No. 1e-64;
Matches 202; Conservative 18; Mismatches 19; Indels 3; Gaps 1;

Qy      1 QVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMGVNQAPKGLEWVSSISGSRITY 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 EVQLVETGGGLVQPGGSLRLSCAASGFTSSYAMSVNQAPKGLEWVAISGSGSTY 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIVYYCAKMDAGSYNFWGQGLTVVSSG 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIVYYCAK--GWRGVDYWRGGLTVVSSG 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      121 GGGSGGGGGGGSETTLTQSPFSLAFVGDRTITTCRASPGIRNYLAWYQOKPGAPYL 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      118 GGGSGGGGGGGSDIQMTQSPSTLSASIGDRVTTCRASGEGYHMLAWYQOKPGAPYL 177
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      181 LIYAATLQSGVPSRFGSGSGTDFTLTISLQPEDPATYVCCQYNSYPLSPFGGTKVEI 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      178 LIYKASSLASGAPSRFGSGSGTDFTLTISLQDPDFATYVCCQYNSYPLSPFGGTKLEI 237
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      241 KR 242
Db      238 KR 239

RESULT 8
US-10-293-418-1922
; Sequence 1922, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2

```

```

; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1922
; LENGTH: 239
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-293-418-1922

Query Match      83.5%; Score 1058.5; DB 15; Length 239;
Best Local Similarity 83.5%; Pred. No. 1e-64;
Matches 202; Conservative 18; Mismatches 19; Indels 3; Gaps 1;

Qy      1 QVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMGVNQAPKGLEWVSSISGSRITY 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 EVQLVETGGGLVQPGGSLRLSCAASGFTSSYAMSVNQAPKGLEWVAISGSGSTY 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIVYYCAKMDAGSYNFWGQGLTVVSSG 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 ADSVKGRTISRDNKNTLYIQMNSLRADTAIVYYCAK--GWRGVDYWRGGLTVVSSG 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      121 GGGSGGGGGGGSETTLTQSPFSLAFVGDRTITTCRASPGIRNYLAWYQOKPGAPYL 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      118 GGGSGGGGGGGSDIQMTQSPSTLSASIGDRVTTCRASGEGYHMLAWYQOKPGAPYL 177
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      181 LIYAATLQSGVPSRFGSGSGTDFTLTISLQPEDPATYVCCQYNSYPLSPFGGTKVEI 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      178 LIYKASSLASGAPSRFGSGSGTDFTLTISLQDPDFATYVCCQYNSYPLSPFGGTKLEI 237
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      241 KR 242
Db      238 KR 239

RESULT 9
US-09-880-748-1882
; Sequence 1882, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1882

```







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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2005, 16:32:07 ; Search time 27.2746 Seconds

(without alignments)  
853.705 Million cell updates/sec

Title: US-09-250-056B-2

Perfect score: 1267

Sequence: 1 QVQLVSGGGLVPGGSLRL.....QQYNISYPLSFGGKVEIKR 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	717	56.6	268	A56446	Ig heavy chain V r
2	701.5	55.4	269	S41374	single chain Fv an
3	628.5	49.6	233	UC5322	p53 specific singl
4	540	42.6	119	S31107	Ig heavy chain - h
5	534	42.1	119	C36005	Ig heavy chain V r
6	533	42.1	119	D36005	Ig heavy chain V r
7	526	41.5	138	S31666	Ig heavy chain V r
8	524.5	41.4	141	S31669	Ig heavy chain V r
9	524	41.4	125	S31051	Ig heavy chain V r
10	523	41.3	119	S31108	Ig heavy chain - h
11	522	41.3	127	S38489	Ig heavy chain - h
12	522	41.2	140	S31686	Ig heavy chain V r
13	520	41.0	140	S31588	Ig heavy chain V r
14	517.5	40.8	120	S48798	Ig heavy chain V r
15	517	40.8	123	S31114	Ig heavy chain - h
16	517	40.8	160	S05271	Ig heavy chain pre
17	512.5	40.4	124	S20782	Ig heavy chain V r
18	507	40.0	133	S23624	Ig heavy chain V r
19	505	39.9	135	S31598	Ig heavy chain V r
20	504.5	39.8	140	S70442	Ig heavy chain pre
21	502.5	39.7	122	S20772	Ig heavy chain V r
22	502	39.6	121	S20772	Ig heavy chain V r
23	500.5	39.5	120	S44111	Ig heavy chain - h
24	499.5	39.4	114	S44111	Ig heavy chain V-D
25	499.5	39.4	128	S26790	Ig heavy chain - h
26	498	39.3	132	S40334	Ig heavy chain V r
27	497	39.2	121	S19666	Ig kappa chain - h
28	496	39.1	109	PH1649	Ig heavy chain V r
29	495	39.1	134	S31699	Ig heavy chain V r

30	494.5	39.0	112	2	PH1647	Ig heavy chain V r
31	494	39.0	121	2	G36005	Ig heavy chain V r
32	493	38.9	119	2	F36005	Ig heavy chain V r
33	493	38.9	120	2	S36278	Ig heavy chain V r
34	491.5	38.8	147	2	I37780	Ig variable region
35	491	38.8	117	2	S34012	Ig heavy chain V r
36	490.5	38.7	118	2	S31105	Ig heavy chain (su
37	490.5	38.7	128	2	S26786	Ig heavy chain V r
38	490.5	38.7	151	2	A60943	Ig heavy chain pre
39	490	38.7	123	2	S26794	Ig heavy chain V r
40	490	38.7	139	2	I37781	Ig variable region
41	489	38.6	121	2	S31104	Ig heavy chain (su
42	488	38.5	108	2	S19674	Ig kappa chain V r
43	488	38.5	127	2	S19878	Ig heavy chain V r
44	488	38.5	134	2	S31679	Ig heavy chain V r
45	487.5	38.5	122	2	S31117	Ig heavy chain - h

## ALIGNMENTS

## RESULT 1

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996

C/Accession: A56446

R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident

A/Reference number: A56446; PMID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TAN>

A/Cross-references: GB:U20617

C/Keywords: heterotetramer; immunoglobulin

Query Match Score 717, DB 2; Length 268;

Best Local Similarity 56.2%; Pred. No. 4.6e-44;

Matches 136; Conservative 40; Mismatches 64; Indels 2; Gaps 2;

Qy	1	QVQLVSGGGLVPGGSLRLSCAASGFTSSYAMGVROAPGKLEWVSSISGSSRYIYV 60
Db	3	QVQLQSGAEIVRPGASVLSCTSGFNKIDITMHWVKRPEGLEWIGRIANAGITKY 62
Qy	61	ADSVKGRFTISRDNSKNTLYLQMNSIADPTAVYYCAKMDAGSYFNFGQGLVTVSSG 120
Db	63	DPKFGKATTAADTSSNTAVYQLSLTSEDTAVYYCASYYLT-RYENYWGQGTIVVSSG 121
Qy	121	GGSGGGGGSGGGSEFTLQSPSFSAFVGDRTITICRASPGIRNYLAWYQGRAPKL 180
Db	122	GGSGGGGSDSGGSDIELTQSPALWASLAEKVTSCRASSV-NFTYMQQSDASPKL 180
Qy	181	LIIYAASLTQGVPSRPSGSGGTFTLTITISLPEDPATYCCQVNSYPLSFGGKVEI 240
Db	181	WVYITHTLPKGVAPARTSGSGSGSYSLTISWMGEDAATYCCQPFSSPTFGSGTLEI 240
Qy	241	KR 242
Db	241	KR 242

## RESULT 2

S41374  
single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995

C/Accession: S41374

R/Artsekenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antibo











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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 19, 2005, 16:24:02 ; Search time 117.033 Seconds  
(without alignments)  
1058.876 Million cell updates/sec

Title: US-09-250-056b-2

Perfect score: 1267  
Sequence: 1 QVQLVSGGGLVPGGSLRL.....QQYNYSPLSGFGTKVEIKR 242

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1023	80.7	240	2 Q65ZC9	Q65ZC9 homo sapien
2	893	70.5	255	2 Q6KB05	Q6KB05 mus musculu
3	874.5	69.0	298	2 Q9QYF0	Q9QYF0 synthetic c
4	864	68.2	244	2 Q65ZC8	Q65ZC8 homo sapien
5	815.5	64.4	248	2 Q65ZQ7	Q65ZQ7 mus sp. b3f
6	745	58.8	241	2 Q921A6	Q921A6 mus musculu
7	733	57.9	243	2 Q7TQM2	Q7TQM2 mus musculu
8	727	57.4	487	2 Q65ZL2	Q65ZL2 mus sp. fv/
9	598.5	47.2	218	2 Q92S51	Q92S51 mus musculu
10	522	41.2	597	2 Q96B89	Q96B89 homo sapien
11	502.5	39.7	118	2 Q9UL91	Q9UL91 homo sapien
12	498	39.3	473	2 Q6MZV7	Q6MZV7 homo sapien
13	495.5	39.1	613	2 Q8WUK1	Q8WUK1 homo sapien
14	494.5	39.0	494	2 Q96K68	Q96K68 homo sapien
15	494	39.0	464	2 Q6MZU6	Q6MZU6 homo sapien
16	491.5	38.8	470	2 Q6PJA4	Q6PJA4 homo sapien
17	489.5	38.6	606	2 Q6GMV2	Q6GMV2 homo sapien
18	489	38.6	121	2 Q9UL71	Q9UL71 homo sapien
19	488	38.5	113	2 Q9UL90	Q9UL90 homo sapien
20	488	38.5	236	2 Q6PIH7	Q6PIH7 homo sapien
21	487.5	38.5	472	2 Q6N0H9	Q6N0H9 homo sapien
22	482.5	38.1	478	2 Q6PI81	Q6PI81 homo sapien
23	482	38.0	573	2 Q6WJ38	Q6WJ38 homo sapien
24	481	38.0	475	2 Q6MZ06	Q6MZ06 homo sapien
25	477	37.6	116	2 Q9UL93	Q9UL93 homo sapien
26	472.5	37.3	122	1 HV3B_HUMAN	Q9UL93 homo sapien
27	471	37.2	115	1 HV3D_HUMAN	P01765 homo sapien
28	468.5	37.0	122	2 Q9UL84	Q9UL84 homo sapien
29	466	36.8	108	2 Q9UL70	Q9UL70 homo sapien
30	466	36.8	236	2 Q6GMX8	Q6GMX8 homo sapien
31	465.5	36.7	114	1 HV3B_HUMAN	P01763 homo sapien

32	463	36.5	117	1 HV3C_HUMAN	P01764 homo sapien
33	462.5	36.5	118	2 Q9UL72	Q9UL72 homo sapien
34	462.5	36.5	147	2 Q9Y509	Q9Y509 homo sapien
35	462	36.5	465	2 Q6P6C4	Q6P6C4 homo sapien
36	462	36.5	485	2 Q6PDB8	Q6PDB8 mus musculu
37	461	36.4	544	2 Q6P095	Q6P095 mus musculu
38	460.5	36.3	466	2 Q6IN78	Q6IN78 homo sapien
39	459.5	36.3	487	2 Q99XA4	Q99XA4 mus musculu
40	458	36.1	108	1 KVI1_HUMAN	P04430 homo sapien
41	458	36.1	236	2 Q6GMX9	Q6GMX9 homo sapien
42	458	36.1	475	2 Q6GMV7	Q6GMV7 homo sapien
43	456	36.0	119	2 Q920E7	Q920E7 mus musculu
44	455.5	36.0	479	2 Q6MZV6	Q6MZV6 homo sapien
45	455	35.9	493	2 Q6GMX2	Q6GMX2 homo sapien

## ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	240 AA.
ID Q65ZC9			
AC Q65ZC9			
DT 25-OCT-2004 (TREMBLrel. 28, Created)			
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE Single-chain Fv (Fragment).			
GN Name=scrFv;			
OS Homo sapiens (human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX NCBI_TaxId=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRATIN=C1q/7;			
RA MEDLINE=97362799; PubMed=9219263;			
RX Kontermann R.E., Wing M.G., Winter G.;			
RT "Complement recruitment using bispecific diabodies.";			
RL Nat. Biotechnol. 15:629-631(1997).			
DR EMBL: Y13056; CAA73499.1; -.			
DR InterPro: IPR003599; IG.			
DR InterPro: IPR007110; IG-like.			
DR InterPro: IPR003596; IG_V.			
DR Pfam: PF00047; IG_2.			
DR SMART: SM00406; IGY_2.			
DR SMART: PSS0835; IG_LIKE; 2.			
DR PROSITE: PSS0835; IG_LIKE; 2.			
FT NON TER 1			
FT 240			
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;			

Query Match 80.7%; Score 1023; DB 2; Length 240;  
Best Local Similarity 81.8%; Pred. No. 4.8e-73;  
Matches 198; Conservative 16; Mismatches 26; Indels 2; Gaps 1;

QY 1 QVQLVSGGGLVPGGSLRLSCAASGTPPSYAMGVRAPGKLEWVSISGSSKYY 60	
DB 1 QVQLVSGGGLVPGGSLRLSCAASGTPPSYAMGVRAPGKLEWVSISGSSKYY 60	
QY 61 ADSVKRFTISRDNSKNTLYIQNLSLRADTVVYCAKMDASGYEFNFGGTLTVSSG 120	
DB 61 ADSVKRFTISRDNSKNTLYIQNLSLRADTVVYCAR--DWGDSLPDPAKGTLYTVSSG 118	
QY 121 GGGSGGGSGGGSGSETTLTQSPSFSAFVGDRTITTCRAAPGIRNYLAAQYKPAAPL 180	
DB 119 GGGSGGGSGGGSGSDIQMTQSPSTLSASIGDVTITTCRASEGIYRWLAWYQKPGAPPL 178	
QY 181 LTYAATLQSGVPSRFGSGSGGTDFLTITSLQPEDFATYYCOQVYSPLSGFGTKVRI 240	
DB 179 LTYKASSLASRAAPSRFGSGSGGTDFLTITSLQPDPAFYIYCOQVSNVLTTCGGLKEI 238	
QY 241 K 242	
DB 241 K 242	

Db 239 KR 240

## RESULT 2

ID Q6KB05 PRELIMINARY; PRT; 255 AA.

AC Q6KB05; 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE SCFV B85 protein (Fragment).  
 GN Name=SCFV B85;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RX NCBI\_TaxID=10090;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=Balb/c;

RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,

RI Briland J.P., Hebeke J.; Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

RL EMBL: A7746180; CAG34081.1; -.

DR HSSP; P01837; 1KCR.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig\_Like.

DR InterPro; IPR003596; Ig\_V.

DR SMART; SM00409; Ig\_2.

DR SMART; SM00406; IgV\_2.

DR PROSITE; PS50835; Ig\_Like; 2.

DR NON TER 1

SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DP713B CRC64;

Query Match 70.5%; Score 893; DB 2; Length 255;

Best Local Similarity 66.3%; Pred. No. 9.8e-63;

Matches 167; Conservative 36; Mismatches 35; Indels 14; Gaps 3;

QY 1 QVQLVSGGGLVPGGSLRLSCAASGFTFSYAMGWROAPKGLEWVSISGSSRYYY 60

Db 1 QVQLQSGGGLVPGGSLRLSCAASGFTFSYAMGWROAPKGLEWVSISGSSRYYY 60

QY 61 ADSVKRFTISRDNSKNTLYLQMNSLRAPETAVYYCA-----KMDASGTFNMGCTLV 115

Db 61 PDSVKRFTISRDNSKNTLYLQMNSLRAPETAVYYCA-----KMDASGTFNMGCTLV 115

QY 116 TVSSGGSGGGSGGGSGSETTLTQSPFSLAFVGDRIITTCRASPGI-----RNYLAW 169

Db 116 TVSSGGSGGGSGGGSGSETTLTQSPFSLAFVGDRIITTCRASPGI-----RNYLAW 169

QY 118 TVSSGGSGGGSGGGSGSETTLTQSPFSLAFVGDRIITTCRASPGI-----RNYLAW 177

Db 118 TVSSGGSGGGSGGGSGSETTLTQSPFSLAFVGDRIITTCRASPGI-----RNYLAW 177

QY 170 YQQRPGKAPLLIYAASTLQSGVPSRPSGSGGTDFTLTITSLQPEDPATYYCOQVNSYP 229

Db 178 YQQRPGKAPLLIYAASTLQSGVPSRPSGSGGTDFTLTITSLQPEDPATYYCOQVNSYP 229

QY 230 LSTFGGTVKIK 241

Db 238 LTFGAGTKLEIK 249

QY 230 LSTFGGTVKIK 241

Db 238 LTFGAGTKLEIK 249

QY 230 LSTFGGTVKIK 241

Db 238 LTFGAGTKLEIK 249

QY 230 LSTFGGTVKIK 241

Db 238 LTFGAGTKLEIK 249

QY 230 LSTFGGTVKIK 241

Db 238 LTFGAGTKLEIK 249

QY 230 LSTFGGTVKIK 241

Db 238 LTFGAGTKLEIK 249

QY 230 LSTFGGTVKIK 241

Db 238 LTFGAGTKLEIK 249

QY 230 LSTFGGTVKIK 241

Db 238 LTFGAGTKLEIK 249

QY 230 LSTFGGTVKIK 241

Db 238 LTFGAGTKLEIK 249

QY 230 LSTFGGTVKIK 241

Db 238 LTFGAGTKLEIK 249

QY 230 LSTFGGTVKIK 241

Db 238 LTFGAGTKLEIK 249

QY 230 LSTFGGTVKIK 241

Db 238 LTFGAGTKLEIK 249

QY 230 LSTFGGTVKIK 241

Db 238 LTFGAGTKLEIK 249

QY 230 LSTFGGTVKIK 241

RA Shinohara N., Demura T., Fukuda H.;

RI "Isolation of a vascular cell wall-specific monoclonal antibody

RT recognizing a cell polarity by using a phase display subtraction

RT method.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).

DR EMBL; AB036341; BAA88633.1; -.

DR FIR; A33933; A33933.

DR FIR; S19112; S19112.

DR HSSP; P01820; 1A70.

DR InterPro; IPR007110; Ig-Like.

DR InterPro; IPR003596; Ig\_V.

DR SMART; SM00406; IgV\_2.

DR PROSITE; PS50835; Ig\_Like; 2.

DR NON TER 1

SQ SEQUENCE 298 AA; 31867 MW; E0F968BA17004317 CRC64;

Query Match 69.0%; Score 874.5; DB 2; Length 298;

Best Local Similarity 67.8%; Pred. No. 3.4e-61;

Matches 166; Conservative 31; Mismatches 41; Indels 7; Gaps 2;

QY 1 QVQLVSGGGLVPGGSLRLSCAASGFTFSYAMGWROAPKGLEWVSISGSSRYYY 60

Db 40 QVQLQSGGGLVPGGSLRLSCAASGFTFSYAMGWROAPKGLEWVSISGSSRYYY 99

QY 61 ADSVKRFTISRDNSKNTLYLQMNSLRAPETAVYYCAKMDASGTFNMGCTLV 117

Db 100 TDSLKDKFTISRDNSKNTLYLQMNSLRAPETAVYYCAKMDASGTFNMGCTLV 155

QY 118 SSGGGSGGGSGGGSGSETTLTQSPFSLAFVGDRIITTCRASPGIRNYLAWYQKPGRA 177

Db 156 SSGGGSGGGSGGGSGSETTLTQSPFSLAFVGDRIITTCRASPGIRNYLAWYQKPGRA 215

QY 178 PKLLIYAASTLQSGVPSRPSGSGGTDFTLTITSLQPEDPATYYCOQVNSYP 237

Db 216 PKLLIYAASTLQSGVPSRPSGSGGTDFTLTITSLQPEDPATYYCOQVNSYP 275

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Db 276 LEIKR 280

QY 238 VEIKR 242

Matches 163; Conservative 39; Mismatches 39; Indels 4; Gaps 2;

QY 1 QYOLVSGGGLVOPGGSLRLSCAASGFTSSYAMGWAPGKLEWVSISGSSRYIY 60  
 DB 1 QYOLVSGGGLVOPGGSLRLSCAASGFTSSYAMGWAPGKLEWVSISGSSRYIY 60

QY 61 ADSVKGRTISRDNSKNTLYLQWNSLRADTAAYVYCAKMDASGSY--FNFMGQGLTVY 117  
 DB 61 AGRFQGRVMTNRTDTSISAAYMEVSRLRSDTAAYVYCAR-EGTGSALYGMQVWGQGLTVY 119

QY 118 SSGGGGGGGGGGGGGGGGGSETTLTOSPSFLSAFVGDRTITTCRAPGIRNTIAYVQKRGKA 177  
 DB 120 SSGGGGGGGGGGGGGGGGGSDIQMTOSPSFLSAFVGDRTITTCRAPGIRNTIAYVQKRGKA 179

QY 178 PKLLIYAASLTOSGVPSPFSGSGGTDFTLTISLQPEPATYVYCOQYNSYPLSPFGGCTK 237  
 DB 180 PFKLLIYKASLSAGAPSPFSGSGGTDFTLTISLQPEPATYVYCOQYNSYPLSPFGGCTK 239

QY 238 VEIKR 242  
 DB 240 LEIKR 244

RESULT 5  
 ID 065207 PRELIMINARY; PRT; 248 AA.

AC 065207;  
 DT 25-OCT-2004 (Tremblrel. 28, Created)  
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
 DE B3(FV)-PE40 (Fragment).  
 GN Name=B3 (FV)-PE40;  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10095;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92020904; PubMed=1924323;  
 RA Britkman U., Pai L.H., Fitzgerald D.J., Williamson M., Pastan I.;  
 RT "B3(FV)-PE38KDEL, a single-chain immunotoxin that causes complete  
 regression of a human carcinoma in mice."  
 RT Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).  
 RL EMBL: S57990; AAB19971.2; -.  
 DR EMBL: IPR003599; Ig\_Like.  
 DR InterPro: IPR007110; Ig\_Like.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_2.  
 DR SMART: SM00409; Ig; 2.  
 DR SMART: SM00406; IGV; 2.  
 DR PROSITE: PS50835; IG\_Like; 2.  
 FT NON\_TER 248 248  
 SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 64.4%; Score 815.5; DB 2; Length 248;  
 Best Local Similarity 64.5%; Pred. No. 1.3e-56;  
 Matches 158; Conservative 29; Mismatches 53; Indels 5; Gaps 1;

QY 2 VOLVSGGGLVOPGGSLRLSCAASGFTSSYAMGWAPGKLEWVSISGSSRYIY 61  
 DB 3 VKLVSGGGLVOPGGSLRLSCAASGFTSSYAMGWAPGKLEWVSISGSSRYIY 62

QY 62 DSVKGRFTISRDNSKNTLYLQWNSLRADTAAYVYCAKMDASGSYFNPWGQGLTVYSSG 121  
 DB 63 DTVKGRFTISRDNSKNTLYLQWNSLRADTAAYVYCAKMDASGSYFNPWGQGLTVYSSG 122

QY 122 GSGGGGGGGGGGGGGGGGGSETTLTOSPSFLSAFVGDRTITTCRAPGIRNTIAYVQKRGKA 176  
 DB 123 GSGGGGGGGGGGGGGGGGGSDIQMTOSPSFLSAFVGDRTITTCRAPGIRNTIAYVQKRGKA 182

QY 177 APKLLIYAASLTOSGVPSPFSGSGGTDFTLTISLQPEPATYVYCOQYNSYPLSPFGGCT 236  
 DB 183 SPKLLIYKASLSAGAPSPFSGSGGTDFTLTISLQPEPATYVYCOQYNSYPLSPFGGCT 242

QY 237 KVEIK 241  
 DB 243 KLEIK 247

RESULT 6  
 ID 0921A6 PRELIMINARY; PRT; 241 AA.

AC 0921A6;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Anti-CEA 79 single chain Fv (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98170165; PubMed=9509426;  
 RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,  
 Yi K.S., Sun P.G., Ryu S.H., Chung H.K.;  
 RT "Cloning and characterization of cDNAs encoding VH and VL of a  
 monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and  
 generation of a single-chain Fv molecule (scFv)."  
 RL Mol. Cells 7:816-819(1997).  
 DR EMBL: U88067; AAB48044.1; -.  
 DR PIR: S19965; S19965.  
 DR PIR: S19967; S19967.  
 DR PIR: S19968; S19968.  
 DR PIR: S26325; S26325.  
 DR HSSP: P01607; IBMW.  
 DR SMART: SM00406; IGV; 2.  
 DR PROSITE: PS50835; IG\_Like; 2.  
 FT NON\_TER 241 241  
 SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 58.8%; Score 745; DB 2; Length 241;  
 Best Local Similarity 57.7%; Pred. No. 4.7e-51;  
 Matches 142; Conservative 42; Mismatches 52; Indels 10; Gaps 4;

QY 1 QYOLVSGGGLVOPGGSLRLSCAASGFTSSYAMGWAPGKLEWVSISGSSRYIY 60  
 DB 1 QYOLVSGGGLVOPGGSLRLSCAASGFTSSYAMGWAPGKLEWVSISGSSRYIY 60

QY 61 ADSVKGRTISRDNSKNTLYLQWNSLRADTAAYVYCAKMDASGSYFNPWGQGLTVYSSG 120  
 DB 61 ADDFKRFAFSLSTASTAYLQWNSLRADTAAYVYCAKMDASGSYFNPWGQGLTVYSSG 119

QY 121 GSGGGGGGGGGGGGGGGGGSETTLTOSPSFLSAFVGDRTITTCRAPGIRNTIAYVQKRGKA 179  
 DB 120 GSGGGGGGGGGGGGGGGGGSDIQMTOSPSFLSAFVGDRTITTCRAPGIRNTIAYVQKRGKA 179

QY 180 ---LLIYAASLTOSGVPSPFSGSGGTDFTLTISLQPEPATYVYCOQYNSYPLSPFGGCT 236  
 DB 180 ARTLHY----IOPGSPFSGSGGTDFTLTISLQPEPATYVYCOQYNSYPLSPFGGCT 234

QY 237 KVEIK 242  
 DB 235 KLEIK 240

RESULT 7  
 ID 07TOM2 PRELIMINARY; PRT; 243 AA.

AC 07TOM2;  
 DT 01-OCT-2003 (Tremblrel. 25, Created)  
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE ScFv 6H8 protein (Fragment).  
 GN Name=scFv 6H8;

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Balb/C;  
 RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;  
 RA Peter J.C., Eftekhari P., Billwald P., Wallukat G., Hoebeke J.;  
 RT "necy single chain antibody variable fragment as inverse agonist for  
 the beta-2 adrenergic receptor.";  
 RL J. Biol. Chem. 278:36740-36747(2003).  
 DR EMBL; AJ574851; CAE00495.1; -.  
 DR HSSP; P01751; 1A6W.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR NON TER 1  
 FT SEQUENCE 243 AA; 25976 MW; BEPFF64D2DCFAF76 CRC64;

Query Match 57.9%; Score 733; DB 2; Length 243;  
 Best Local Similarity 58.9%; Pred. No. 4.2e-50; Indels 4; Gaps 2;  
 Matches 142; Conservative 39; Mismatches 56;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFSYAMGVWROAPGKLEWVSISGSSRYIY 60  
 DB 1 QVQLQSGSEIVRPGASVLTSCASGYTTFTTVMHWVKQRHGGGLMIGNITYPGSGITNY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADPTAVYICAKMDAGSYNPFNGGTLVTSSG 120  
 DB 61 DEKFKKKGILVTDTSSSTAYMHLSSLSSEDSAVYFCAR--GGRGADVAGAGTTLTVSSG 117  
 QY 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 180  
 DB 118 GGGSGGGSGGGSDIQMTQSSSFVSLSGDRVLTTCASSEDITYNLAWYQKPGKAPKL 177  
 QY 181 LIYAATLQSGVPSRPSGSGGTDFTLTISLQPEDFATYCCQVNSYPLSFGGKTVEI 240  
 DB 178 LLSGATSLRGTGVSRRSGSGSKDYLTSLTQTEVAVTYCCQVNS-TRTFGGKRLKI 236  
 QY 241 K 241  
 DB 237 K 237

## RESULT 8

Q652L2 PRELIMINARY; PRT; 487 AA.  
 ID Q652L2;  
 AC Q652L2;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE FV/M4.  
 GN Name=M4-IFN- $\langle$ tau $\rangle$ ;  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=96272580; PubMed=8688499;  
 RA O. Y., Xiang J.;  
 RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric  
 antibody secreted from myeloma cells.";  
 RL Hum. Antibodies Hybridomas 6:161-166(1995).  
 DR EMBL; S82493; AAB37424.2; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003597; IG\_cl.  
 DR InterPro; IPR003598; IG\_c2.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.

DR Pfam; PF07654; Cl-act; 2.  
 DR Pfam; PF00047; IG; 4.  
 DR SMART; SM00409; IG; 3.  
 DR SMART; SM00407; IGcl; 2.  
 DR SMART; SM00408; IGC2; 2.  
 DR SMART; SM00406; IGV; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 DR SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match 57.4%; Score 727; DB 2; Length 487;  
 Best Local Similarity 56.4%; Pred. No. 2.7e-49; Indels 6; Gaps 2;  
 Matches 136; Conservative 43; Mismatches 56;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTFSYAMGVWROAPGKLEWVSISGSSRYIY 60  
 DB 20 QVQLQSGDAELVKGPAVSXISCKAGSYTTHDAIHMAKQKPGGLEWIGYISPGNDIKY 79  
 QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADPTAVYICAKMDAGSYNPFNGGTLVTSSG 120  
 DB 80 NEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVYFCR-----SYGHWGGGTTTLT-GSG 133  
 QY 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 180  
 DB 134 GGGSGGGSGGGSRITQMTQSSSVSLVGLVLTTCRASSENITYNLAWYQKQKGSFOL 193  
 QY 181 LIYAATLQSGVPSRPSGSGGTDFTLTISLQPEDFATYCCQVNSYPLSFGGKTVEI 240  
 DB 194 LIYAATNLADGVPSRRSGSGGTQVSLKINLSQSEDFGTYCQHFMTGTFTYGGGRLKI 253  
 QY 241 K 241  
 DB 254 K 254

## RESULT 9

Q925S1 PRELIMINARY; PRT; 218 AA.  
 ID Q925S1;  
 AC Q925S1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE MKP5 (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Balb/C;  
 RX PubMed=11819679;  
 RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,  
 Su C.;  
 RT "Mechanism of exogenous nucleic acids and their precursors improving  
 the repair of intestinal epithelium after irradiation in mice.";  
 RL World J. Gastroenterol. 6:709-717(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Balb/C;  
 RA Cui D., Zeng G., Yan X., Li X., Su C.;  
 RT "Cloning of mouse genes related to repairing of intestinal epithelium  
 of the irradiated mice by treatment with the intestinal RNA of mice of  
 the same strain.";  
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).  
 DR EMBL; AF240168; AAK43733.1; -.  
 DR HSSP; P01665; 1QNZ.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR NON TER 218  
 FT SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 47.2%; Score 598.5; DB 2; Length 218;  
 Best Local Similarity 53.5%; Pred. No. 1.6e-39;



Matches 116; Conservative 38; Mismatches 58; Indels 5; Gaps 2;

QY 1 QVQLVSGGGLVOPGSLRLSCAASGFTSSYAMGVWROAPGKLEWVSISGSSRYYY 60  
 DB 3 QVQLVSGGGLVOPGSLRLSCAASGFTSSYAMGVWROAPGKLEWVSISGSSRYYY 62  
 QY 61 ADSVKRFTISRDNSKNTLYLQNSLRADDTAVYYCAKADASGSYFNFGQGLTVYSSG 120  
 DB 63 ABEFKRFPFSLTSTASTAYLQISNLKNEDTATYFCRMWDYDGG-FAVWQGGTTLTVYSSG 121  
 QY 121 GGGSGGGGSGGGSETTLTQSPSFLSAFVGDRTITTCRASPGIRN-----YLAWYQOKPK 176  
 DB 122 GGGSGGGGSGGGSDYVLTIQSPSLAVSLGQRAITISGRASESVDNIGISFMMWFQOKPKG 181  
 QY 177 APRLLIYAASTLQSGVPSRPSGSGGTDTTLTISIQ 213  
 DB 182 PPKLLIYAAASKGSGVPAAGLLASGSGTDFSLNIYPM 218

## RESULT 10

ID Q96BB9 PRELIMINARY; PRT; 597 AA.  
 AC Q96BB9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE IGHM protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.L., Hong L.,  
 RA Stajich E., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalak U., Smalms D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 DB EMBL, BC015760, AAH15760.1; -

DR EMBL, BC015760, AAH15760.1; -  
 DR PIR, S05271, S05271.  
 DR PIR, S24260, S24260.  
 DR HSSP, P01861, IADQ.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig-cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; Cl-sect; 4.  
 DR SMART: SM00406; Igy; 1.  
 DR PROSITE: PSS0835; IG\_LIKE; 5.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_3.  
 DR PROSITE: 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;  
 SQ SEQUENCE

Query Match 41.2%; Score 522; DB 2; Length 597;  
 Best Local Similarity 64.4%; Pred. No. 5, 6e-33;  
 Matches 114; Conservative 12; Mismatches 19; Indels 32; Gaps 5;

QY 1 QVQLVSGGGLVOPGSLRLSCAASGFTSSYAMGVWROAPGKLEWVSISGSSRYYY 60  
 DB 20 QVQLVSGGGLVOPGSLRLSCAASGFTSSYAMGVWROAPGKLEWVSISGSSRYYY 79  
 QY 61 ADSVKRFTISRDNSKNTLYLQNSLRADDTAVYYCAK-----MDASGSYF--NFGQGLT 114  
 DB 80 ADSVKRFTISRDNSKNTLYLQNSLRADDTAVYYCAKAPRGASAGNTREDYWGQGLT 139  
 QY 115 VYVSSGGGGSGGGSGGGSETTL-----TQSPSFLSA-----FVGDRIIT 156  
 DB 140 VYVSS-----GSASAPFLFVLVSCENSPSDTSSVAVAGCLAQDFLSDITS 185

## RESULT 11

ID Q9UL91 PRELIMINARY; PRT; 118 AA.  
 AC Q9UL91;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjln.1998.4531;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus.";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL, AF035023; AAD56259.1; -  
 DR PIR, PH0875; PH0875.  
 DR PIR, S21205; S21205.  
 DR PIR, S30531; S30531.  
 DR HSSP, P01783; IIGC.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_v.  
 DR SMART: SM00406; Igy; 1.  
 DR PROSITE: PSS0835; IG\_LIKE; 1.  
 DR NON TER 1  
 FT NON TER 118  
 SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 39.7%; Score 502.5; DB 2; Length 118;  
 Best Local Similarity 83.1%; Pred. No. 3, 2e-32;  
 Matches 98; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 1 QVQLVSGGGLVOPGSLRLSCAASGFTSSYAMGVWROAPGKLEWVSISGSSRYYY 60  
 DB 1 QVQLVSGGGLVOPGSLRLSCAASGFTSSYAMGVWROAPGKLEWVSISGSSRYYY 60  
 QY 61 ADSVKRFTISRDNSKNTLYLQNSLRADDTAVYYCAKADASGSYFNFGQGLTVYSSG 118  
 DB 61 ADSVKRFTISRDNSKNTLYLQNSLRADDTAVYYCAKADASGSYFNFGQGLTVYSSG 117

## RESULT 12

ID Q6MZV7 PRELIMINARY; PRT; 473 AA.  
 AC Q6MZV7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein DKFp686c11235.

GN Name=DKFZp686C11235;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human small intestine;  
 RG The German Human cDNA Consortium;  
 RA Bloeker H., Becher M., Mewes H.W., Weil B., Amlid C., Osanger A.,  
 RA Fobg G., Han M., Wiemann S.;  
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BK640853; CAB45920.1; -  
 DR HSSP; P01861; IADQ.  
 DR InterPro; IPR003599; I9.  
 DR InterPro; IPR007110; I9-like.  
 DR InterPro; IPR003597; I9-cl.  
 DR InterPro; IPR003006; I9\_MHC.  
 DR InterPro; IPR003596; I9\_v.  
 DR Pfam; PF07654; Cl-sec; 3.  
 DR SMART; SM00409; IGV; 2.  
 DR SMART; SM00407; IGV; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IGV\_LIKE; 4.  
 DR PROSITE; PS00290; IGV\_MHC; UNKNOWN\_2.  
 DR Hypothetical protein.  
 SQ SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BFC447 CRC64;

Query Match 39.1%; Score 498; DB 2; Length 473;  
 Best Local Similarity 46.8%; Pred. No. 3.4e-31;  
 Matches 118; Conservative 30; Mismatches 58; Indels 46; Gaps 9;  
 QY 1 QVQLVESGGGLVOPGSLRLSCAASGFTSSYAMGVROAPKGLFEMWSISGSSRYIY 60  
 DB 20 ELQVLESVGGGLVOPGSLRLSCAASGFTSSYFEMNVRQAPKGLFEMLSITTSNTVIY 79  
 QY 61 ADSVKGRTISRDNSKNTLYLQNSLRADTAVVYCAKMDASG--SYFNFWGGGLTV 115  
 DB 80 ADSVKGRTISRDNSKNTLYLQNSLRADTAVVYCAKMDASG--SYFNFWGGGLTV 139  
 QY 116 TVSSGGGGGGGGGGGGSTTTLTQSPFLSAVGRITTCASRG--IRNVLAVYQOK 173  
 DB 140 TVSSASG-----TKGSPVFPPLAPSSKSTSGTAAAGLVKDFL----- 177  
 QY 174 PGKAPKLLIYAASLTQSGV---PSRPSGSG---SGTDFTLTISLQPEDPATYVCOQVNS 227  
 DB 178 ---EPTVWMNSGALISGCHTTPAVVLOSGLYLSVSVTVPPSSLSGTQ---TTC-NVNH 230  
 QY 228 YPLSPGGGTKE 239  
 DB 231 KP-----SNTKVD 238

RESULT 13  
 Q8WUK1 PRELIMINARY; PRT; 613 AA.  
 AC Q8WUK1;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE IGHM protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahay J., Helton E., Kettlemen M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002);  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC020240; AAH20240.1; -  
 DR PIR; F36005; F36005.  
 DR PIR; G36005; G36005.  
 DR PIR; PH1642; PH1642.  
 DR PIR; PH1643; PH1643.  
 DR PIR; PH1645; PH1645.  
 DR PIR; PH1646; PH1646.  
 DR PIR; P10098; P10098.  
 DR PIR; P10120; P10120.  
 DR PIR; S15590; S15590.  
 DR PIR; S31116; S31116.  
 DR PIR; S31119; S31119.  
 DR PIR; S70442; S70442.  
 DR HSSP; P01861; IADQ.  
 DR Pfam; PF07654; Cl-sec; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IGV\_LIKE; 5.  
 DR PROSITE; PS00290; IGV\_MHC; UNKNOWN\_3.  
 SQ SEQUENCE 613 AA; 67295 MW; 60CF5950671E315 CRC64;

Query Match 39.1%; Score 495.5; DB 2; Length 613;  
 Best Local Similarity 64.0%; Pred. No. 7.2e-31;  
 Matches 110; Conservative 8; Mismatches 27; Indels 27; Gaps 4;  
 QY 1 QVQLVESGGGLVOPGSLRLSCAASGFTSSYAMGVROAPKGLFEMWSISGSSRYIY 60  
 DB 20 QVQLVESGGGLVOPGSLRLSCAASGFTSSYGMNVRQAPKGLFEMVAIVSYDSNKTY 79  
 QY 61 ADSVKGRTISRDNSKNTLYLQNSLRADTAVVYCAKMDASG--SYFNFWGGGLTV 119  
 DB 80 ADSVKGRTISRDNSKNTLYLQNSLRADTAVVYCAKMDASGSEVFIDWGGTWTVSS 139  
 QY 120 GGGGGGGGGGGGGSTTTLTQSPFLSA-----FYGDRITTT 156  
 DB 140 -----GSASAPTLFPLVSCENSPDTSVAVGCLAQFLPDSITFS 180

RESULT 14  
 Q96K68 PRELIMINARY; PRT; 494 AA.  
 AC Q96K68;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Hypothetical protein FLJ14473.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;



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